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Scientific and Technical Information Center

SEP 13 2005

SEARCH REQUEST FORM

STIC/TECH/CHEM. DIVISION
(STIC)

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 9-12-05
Art Unit: 1638 Phone Number: 2-0765 Serial Number: 09/896,692
Location (Bldg/Room#): 2D12 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Novel HIV specific oligos.
Inventors (please provide full names): S. AGRAWAL

Earliest Priority Date: 10/29/01

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search

• Seq ID Nos 4 + 5.

• Size limit to 22 Nucleotides.

Interference + regular Database
please.

Thanks.

STAFF USE ONLY

Searcher: _____ Type of Search 2 NA Sequence (#)

Searcher Phone #: _____ AA Sequence (#)

Searcher Location: _____ Structure (#)

Date Searcher Picked Up: 9/13/05 Bibliographic

Completed: 9/15/05 Litigation

Prep & Review Time: _____ Fulltext

_____ Other

Vendors and cost where applicable

_____ STN _____ Dialog

_____ Questel/Orbit _____ Lexis/Nexis

_____ Westlaw _____ WWW/Internet

Q in-house sequence systems

X Commercial _____ Oligomer _____ Score/Length
X Interference _____ SPDI _____ Encode/Transl
Other (specify) _____

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 23:41:57; Search time 1369.12 Seconds
(without alignments)
611.646 Million cell updates/sec

Title: US-09-896-692B-5

Perfect score: 22

Sequence: 1 tcgacccatctctctctctct 22

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 18786

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb-est1:*
2: gb-est2:*
3: gb-htc:*
4: gb-est3:*
5: gb-est4:*
6: gb-est5:*
7: gb-est6:*
8: gb-gsbl:*
9: gb-gsbl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12.2	55.5	22	8	AZ821337 2M0094L04
C 2	12	54.5	21	8	AZ976439 2M0251B24
C 3	12	54.5	22	8	AZ816374 2M0085005
C 4	11.8	53.6	22	9	TA245E10P
C 5	11.2	50.9	16	5	B0588621
C 6	11	50.0	20	8	AZ579532
C 7	11	50.0	20	8	AZ828544
C 8	11	50.0	22	1	A1439277
C 9	11	50.0	22	1	A1688330
C 10	11	50.0	22	8	BH000100
C 11	10.8	49.1	19	8	AZ807034
C 12	10.8	49.1	20	4	BG927393
C 13	10.8	49.1	20	6	CD533465
C 14	10.6	48.2	19	8	AZ432757
C 15	10.6	48.2	20	7	CF932153
C 16	10.6	48.2	21	7	CR753356
C 17	10.6	48.2	21	8	AZ371089
C 18	10.6	48.2	22	8	AZ652627
C 19	10.4	47.3	12	5	B0587766
C 20	10.4	47.3	16	5	B0587767
C 21	10.4	47.3	21	8	AZ819492
C 22	10.4	47.3	22	8	AZ800838
C 23	10.2	46.4	17	1	AJ666397
C 24	10.2	46.4	19	5	B0593604

25	10.2	46.4	19	8	AZ610584
26	10.2	46.4	20	9	CL687844
27	10.2	46.4	21	8	AZ877187
C 28	10.2	46.4	21	9	CL695388
29	10.2	46.4	22	1	A1630912
30	10	45.5	19	8	AZ447414
31	10	45.5	19	9	CL657608
C 32	10	45.5	20	8	AZ388212
33	10	45.5	21	8	AZ309714
34	10	45.5	21	8	AZ798977
35	10	45.5	21	8	AZ830720
36	10	45.5	21	9	AJ587257
37	10	45.5	22	4	BG925518
C 38	10	45.5	22	8	AZ307952
C 39	10	45.5	22	8	AZ640656
40	10	45.5	22	9	TA226C020
41	9.8	44.5	17	5	B0593528
42	9.8	44.5	18	4	BG668047
C 43	9.8	44.5	18	5	B0594437
44	9.8	44.5	19	8	AZ440413
45	9.8	44.5	19	8	AZ489586

ALIGNMENTS

RESULT 1
LOCUS AZ821337/c
DEFINITION 2M0094L04F Mouse 10kb plasmid UUCGIM library Mus musculus genomic
clone UUCG2M0094L04 F, genomic survey sequence.

ACCESSION AZ821337
VERSION AZ821337.1 GI:12991245
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A., and Wright,D.,Weise,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

FEATURES
source
Email: ddmmgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: 1 column: 04
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0094L04"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 55.5%; Score 12.2; DB 8; Length 22;
Best Local Similarity 82.4%; Pred. No. 6.9e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CCCATCTCTCTCT 22
DB 21 CCTATCTCCTCTCT 5

RESULT 2
A2976439 21 bp DNA linear GSS 27-APR-2001
LOCUS 2M025124R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION Clone UUGC2M0251B24 R, genomic survey sequence.
ACCESSION A2976439
VERSION A2976439.1 GI:13847666
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0251 row: B column: 24
Seq primer: CACACGAAACAGCATATACG
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1..21

FEATURES
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1..21
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0251B24"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 54.5%; Score 12; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCCATCTCTCTC 17
DB 4 CCCATCTCTCTC 15

RESULT 3
A2816374 22 bp DNA linear GSS 20-FEB-2001
LOCUS 2M008505F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION Clone UUGC2M0085005 F, genomic survey sequence.
ACCESSION A2816374
VERSION A2816374.1 GI:12986282
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0085 row: O column: 05
Seq primer: CGTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22

FEATURES
source
1..22
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0085005"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 54.5%; Score 12; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.4e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 TCTCTCTCTTC 21
| | | | |
| | | | |
Db 20 TCTCTCTCTTC 9

RESULT 4
TA245E10P/c 22 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 245e10, forward sequence.
DEFINITION genomic survey sequence.
ACCESSION AL483585
VERSION AL483585.1 GI:11849086
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE
AUTHORS Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. E., Rajandream, M. A. and Barrell, B. G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J. C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="245e10"

ORIGIN

Query Match 53.6%; Score 11.8; DB 9; Length 22;
Best Local Similarity 86.7%; Pred. No. 1e+06;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TCGACCACTCTCTC 15

Db 20 TTGCACCACTCTC 6

RESULT 5
B0588621 16 bp mRNA linear EST 06-DEC-2002
DEFINITION E012562-024-015-N03-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
LOCUS cDNA clone 024-015-N03 5-PRIME, mRNA sequence.
ACCESSION B0588621
VERSION B0588621.1 GI:26118204
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehnrich, H. and Radelof, U.
TITLE Construction of a 'uniGene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PMID 12472698

COMMENT
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 15 row: N column: 03
Seq primer: SP6: CATGAGATTAGGTGACACTATAG.

FEATURES
source
1..16
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/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:187387"
/db_xref="taxon:161934"
/clone="024-015-N03"
/tissue_type="storage root"
/lab_host="EMD10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site1: SalI; Site2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzelebeher Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCCG-5p-prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN

Query Match 50.9%; Score 11.2; DB 5; Length 16;
Best Local Similarity 81.2%; Pred. No. 1.8e+06;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4 CACCATCTCTCTCT 19
| | | | |
| | | | |
Db 1 CACTTCTCTCTCT 16

RESULT 6
A2579532 20 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0367H10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0367H10 F, genomic survey sequence.

ACCESSION A2579532
VERSION A2579532.1 GI:11693961
KEYWORDS GSS.
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: H column: 10
Seq primer: CATTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0367H10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 50.0%; Score 11; DB 8; Length 20;
Best Local Similarity 73.7%; Pred. No. 2.2e+06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGACCATCTCTCTCT 19
| | | | | | | | | | | | | | | | | | | | | |
Db 2 TCGTACACACACTCTCT 20

RESULT 7
A2828544 20 bp DNA linear GSS 20-FEB-2001
LOCUS
DEFINITION
c10105004R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0105004 R, genomic survey sequence.

ACCESSION A2828544
VERSION A2828544.1 GI:12998452
KEYWORDS GSS.
SOURCE Mus musculus
ORGANISM Mus musculus (house mouse)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0105 row: O column: 04
Seq primer: CACACAGAAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0105004"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 50.0%; Score 11; DB 8; Length 20;
Best Local Similarity 73.7%; Pred. No. 2.2e+06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGACCATCTCTCTCT 19
| | | | | | | | | | | | | | | | | | | | | |
Db 19 TCTACCCCACTCTGTCT 1

RESULT 8
A1439277 22 bp mRNA linear EST 09-MAR-1999
LOCUS
DEFINITION
U154602.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134250 3'
similar to TR:Q17089 Q17089 COLLAGEN; contains element MER22

repetitive element ; mRNA sequence.

ACCESSION AL439277
VERSION AL439277.1 GI:4303196
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 22)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLNM at: www.bio.llnl.gov/bbtrp/image/image.html

FEATURES
source
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2134250"
/tissue_type="lymphoma, follicular mixed small and large cell"
/lab_host="DH10B"
/clone_lib="NCI-CCAP_Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORE; site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

ORIGIN
Query Match 50.0%; Score 11; DB 1; Length 22;
Best Local Similarity 73.7%; Pred. No. 2.3e+06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CGGACCCATCTCTCTCTT 20
||| ||| ||| ||| |||
Db 3 CGCCCCCACCCCCCTT 21

RESULT 9
AL688330 22 bp mRNA linear EST 17-DEC-1999
LOCUS wc94c08.x1 NCI-CCAP C03 Homo sapiens cDNA IMAGE:2336286 3'
DEFINITION similar to TR:Q64371 Q64371 PR-VBETA1. ;contains element MSK1 repetitive element ; mRNA sequence.
ACCESSION AL688330
VERSION AL688330.1 GI:4899624
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 22)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Benito Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLNM at: www.bio.llnl.gov/bbtrp/image/image.html

Trace considered overall poor quality
Insert Length: 670 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..22
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2326286"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
/clone_lib="NCI-CCAP C03"
/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dt) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization."

ORIGIN
Query Match 50.0%; Score 11; DB 1; Length 22;
Best Local Similarity 73.7%; Pred. No. 2.3e+06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 CACCATCTCTCTCTCTT 22
||| ||| ||| ||| |||
Db 22 CCCCCCTCCCTCTT 4

RESULT 10
BH000100 22 bp DNA linear GSS 27-APR-2001
LOCUS 2M0287A18 Mouse 10kb plasmid U06C2M library Mus musculus genomic
DEFINITION clone U06C2M0287A18 R, genomic survey sequence.
ACCESSION BH000100
VERSION BH000100.1 GI:13871326
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0287 row: A column: 18
Seq primer: CACACAGGAAACAGCTAGAC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22

FEATURES
source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U062M0287A18"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid U062M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 50.0%; Score 11; DB 8; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CTCCTCTCTC 21
Db 22 CTCCTCTCTC 12

RESULT 11
LOCUS AZ807034 19 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0069505R Mouse 10kb plasmid U062M library Mus musculus genomic clone U062M0069505 R, genomic survey sequence.

ACCESSION AZ807034

VERSION AZ807034.1 GI:12970979

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0069 row: B column: 05

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES
SOURCE

1..19

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U062M0069505"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid U062M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 49.1%; Score 10.8; DB 8; Length 19;
Best Local Similarity 85.7%; Pred. No. 2.7e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CACCCATCTCTC 17
Db 18 CTCCTCTCTCTC 5

RESULT 12
LOCUS BG927393 20 bp mRNA linear EST 06-NOV-2001

DEFINITION HNC1-1-F7.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

ACCESSION BG927393

VERSION BG927393.1 GI:14321916

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 20)

REFERENCE

AUTHORS

Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathé,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL

COMMENT

MECLINE

PUBMED

11597177

Contact: Sanjay Kumar

UM2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar@glsk.com

Seq primer: T7.

Location/Qualifiers

1..20

FEATURES
SOURCE
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

ORIGIN

/tissue type="cartilage"
/lab host="E. coli DH10 B"
/clone lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

Query Match 49.1%; Score 10.8; DB 4; Length 20;
Best Local Similarity 85.7%; Pred. No. 2.7e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CACCATCTCTCTC 17
|||||
7 CACCATCTCTCTC 20

RESULT 13
CD533465 21 bp mRNA linear EST 31-DEC-2003
LOCUS 3166 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
DEFINITION 3', mRNA sequence.
ACCESSION CD533465
VERSION CD533465.1 GI:40453477
KEYWORDS EST.
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Guo, Y., Cai, Z. and Gan, S.
TITLE Transcriptome of Arabidopsis leaf senescence
JOURNAL Plant Cell Environ. 27 (5), 521-549 (2004)
COMMENT Department of Horticulture
Cornell University
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
Tel: 607 254 5418
Fax: 607 255 0599
Email: sg288@cornell.edu
Insert Length: 21 Std Error: 0.00
Seq primer: T7
POLYA=No.

FEATURES

Location/Qualifiers

1..21
/organism="Arabidopsis thaliana"
/mol type="mRNA"
/ecotype="landberg erecta"
/db_xref="taxon:3702"
/tissue type="Leaf"
/dev stage="Yellow Leaf With Greenish Base Area"
/lab host="E. coli"
/clone lib="Arabidopsis Leaf Senescence Library"
/note="Organ: Rosette Leaf; Vector: pBluscript SKII+;
Site_1: EcoRI; Site_2: EcoRI; Senescent rosette leaves #5
and #6 (counted from the bottom) were harvested and
immediately frozen in liquid N2. The leaves were visibly
yellow excepted for the leaf base areas that were still
greenish."

ORIGIN

Query Match 49.1%; Score 10.8; DB 6; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.7e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 9 ATCTCTCTCTCTCT 22
|||||
Db 3 ATCTTCTCTTCTTCT 16

RESULT 14
AZ432757/c 19 bp DNA linear GSS 03-OCT-2000

DEFINITION 1M021814F Mouse 10kb plasmid UNGCM library Mus musculus genomic
clone UNGCM021814 F, genomic survey sequence.
ACCESSION AZ432757
VERSION AZ432757.1 GI:10556770
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0218 row: L column: 14
Seq primer: CGTGTAAACGACGCCACAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers

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/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNGCM021814"
/sex="Male"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UNGCM library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114|gb|AF129072.1) a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 48.2%; Score 10.6; DB 8; Length 19;
Best Local Similarity 76.5%; Pred. No. 3.3e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 6 CCATCTCTCTCTCTCT 22
|||||
Db 19 CCTCTCTCTCTCTCTCT 3

RESULT 15
CF932153 20 bp mRNA linear EST 15-MAR-2004

```

DEFINITION  SP1-A4(P6-E4) A suppression subtractive hybridization cDNA library
              from bacterial-blight-resistant cotton Gossypium hirsutum cDNA
              clone SP1-A4(P6-E4), mRNA sequence.
ACCESSION   CP932153
VERSION     CP932153.1
KEYWORDS    GI:45438734
SOURCE      EST.
            Gossypium hirsutum (upland cotton)
ORGANISM    Gossypium hirsutum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosid II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Patil,M.A., Pierce,M.L., Phillips,A.L., Venter,B. and
            Essenberg,M.K.
TITLE       A pursuit of genes active in defense of upland cotton against
            bacterial blight
COMMENT     Unpublished (2004)
            Contact: Margaret Essenberg
            Biochemistry and Molecular Biology
            Oklahoma State University
            246 Noble Research Centre, Stillwater, OK 74078, USA
            Tel: 4057446203
            Fax: 4057447799
            Email: margess@okstate.edu
            Seq primer: REVERSE
FEATURES
  source
    1..20
    location/Qualifiers
      /organism="Gossypium hirsutum"
      /mol_type="mRNA"
      /cultivar="Im216"
      /db_xref="taxon:3635"
      /clone="SP1-A4(P6-E4)"
      /tissue_type="Foliar leaves inoculated with Xanthomonas
      campestris pv. malvacearum 3631"
      /dev_stage="8, 14, 20, 30, 45 and 60 hours post
      inoculation"
      /clone_lib="A suppression subtractive hybridization cDNA
      library from bacterial-blight-resistant cotton"
      /note="Equal quantities of RNA from all stages were
      combined prior to mRNA isolation. In the cDNA subtraction
      procedure, the reference cDNA was from non-inoculated
      leaves"
ORIGIN
Query Match 48.2%; Score 10.6; DB 7; Length 20;
Best local Similarity 76.5%; Pred. NO. 3.3e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 2 CGACCCCATCTCTCTCC 18
    |||||
Db 1 CGCTCCCTTCCCTCCCC 17
    |||||

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Search completed: September 15, 2005, 02:08:15
 Job time : 1370.12 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 23:12:17; Search time 808.372 Seconds
(without alignments)
1318.718 Million cell updates/sec

Title: US-09-896-692B-5
Perfect score: 22
Sequence: 1 tcgcaccatctctctctct 22

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24627607955 residues
Total number of hits satisfying chosen parameters: 952800

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBml:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_strs:*
12: gb_by:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	6	I49132 Sequence 6
2	22	100.0	22	6	BD077067 Novel HIV
3	21	95.5	21	6	I49133 Sequence 7
4	21	95.5	21	6	AX146648 Sequence
5	21	95.5	21	6	AX203700 Sequence
6	21	95.5	21	6	BD077063 Novel HIV
7	21	95.5	21	6	BD077064 Novel HIV
8	21	95.5	21	6	BD077065 Novel HIV
9	21	95.5	21	6	BD077066 Novel HIV
10	21	95.5	21	6	BD077068 Novel HIV
11	20	90.9	20	6	I49134 Sequence 8
12	20	90.9	20	6	AR206325 Sequence
13	20	90.9	21	6	AR374987 Sequence
14	20	90.9	22	6	AR170398 Sequence
15	19.4	88.2	22	6	AR140320 Sequence
16	19.4	88.2	22	6	AR206326 Sequence
17	19.4	88.2	22	6	AR287299 Sequence
18	19	86.4	20	6	A27240 Antiviral D
19	19	86.4	20	6	BD192520 Compositi

20	19	86.4	20	6	I09442 Sequence 6
21	19	86.4	20	6	I72636 Sequence 10
22	19	86.4	20	6	AR260544 Sequence
23	19	86.4	20	6	AR260545 Sequence
24	19	86.4	20	6	AR260561 Sequence
25	19	86.4	22	6	AR430157 Sequence
26	19	86.4	22	6	AX363503 Sequence
27	18.4	83.6	21	6	AR206343 Sequence
28	18	81.8	18	6	AX772003 Sequence
29	17	77.3	17	6	I28579 Sequence 32
30	17	77.3	17	6	I58741 Sequence 32
31	17	77.3	17	6	AR486969 Sequence
32	17	77.3	17	6	AX418589 Sequence
33	17	77.3	17	6	AX552328 Sequence
34	17	77.3	20	6	A45278 Sequence 9
35	17	77.3	20	6	AR055037 Sequence
36	17	77.3	20	6	AR116258 Sequence
37	17	77.3	20	6	AR156286 Sequence
38	16.8	76.4	21	6	AR206344 Sequence
39	16	72.7	19	6	I78667 Sequence 22
40	16	72.7	22	6	AX540488 Sequence
41	15.4	70.0	20	6	AR100320 Sequence
42	15.4	70.0	20	6	AR149975 Sequence
43	15.4	70.0	20	6	BD227848 Antisense
44	15	68.2	18	6	I26577 Sequence 2
45	14.4	65.5	19	6	I78665 Sequence 20

ALIGNMENTS

RESULT 1	I49132	Sequence 6 from patent US 5627277.	22 bp	DNA	linear	PAT 07-OCT-1997
LOCUS	I49132					
DEFINITION	I49132					
ACCESSION	I49132.1	GI:2467595				
VERSION						
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 22)					
AUTHORS	Cohen,A.S., Bourque,A. and Vilenchik,M.					
TITLE	Method for analyzing oligonucleotide analogs					
JOURNAL	Patent: US 5627277-A 6 06-MAY-1997;					
FEATURES	location/Qualifiers					
source	1..22					
ORIGIN	/organism="Unknown"					
	/mol_type="unassigned DNA"					
Query Match	100.0%; Score 22; DB 6; Length 22;					
Best local similarity	100.0%; Pred. No. 4.6;					
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1 TCGCACCATCTCTCTCTCT 22					
Db	1 TCGCACCATCTCTCTCTCT 22					
RESULT 2	BD077067	22 bp	DNA	linear	PAT 27-AUG-2002	
LOCUS	BD077067					
DEFINITION	Novel HIV-specific synthetic oligonucleotide and method of using the same.					
ACCESSION	BD077067.1	GI:22622670				
VERSION						
KEYWORDS	JP 2001514884-A/5.					
SOURCE	Human immunodeficiency virus					
ORGANISM	Human immunodeficiency virus					
REFERENCE	1 (bases 1 to 22)					

AUTHORS Agrawal, S.
TITLE Novel HIV-specific synthetic oligonucleotide and method of using the same
JOURNAL Patent: JP 2001514884-A 5 18-SEP-2001;
HYBRIDON INC

COMMENT OS Human immunodeficiency virus
PN JP 2001514884-A/5
PD 18-SEP-2001
PF 05-AUG-1998 JP 2000509820
PR 19-AUG-1997 US 08/914827
PI SUDHIR AGRAWAL
PC C12N15/09, A61K31/7125, A61P31/18, C12N15/00
CC Novel HIV-specific synthetic oligonucleotide and method of using the same

FEATURES FT Key Location/Qualifiers
FT source 1..22
Location/Qualifiers
1..22
/organism="Human immunodeficiency virus"
/mol_type="genomic DNA"
/db_xref="taxon:12721"

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTCT 22
1 TCGACCCATCTCTCTCTTCT 22

Db 1 TCGACCCATCTCTCTCTTCT 22

RESULT 3
LOCUS I49133 21 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 7 from patent US 5627277.
ACCESSION I49133
VERSION I49133.1 GI:2467596
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Cohen, A.S., Bourque, A. and Vilenchik, M.
TITLE Method for analyzing oligonucleotide analogs
JOURNAL Patent: US 5627277-A 7 06-MAY-1997;
FEATURES Location/Qualifiers
1..21
/organism="Unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGCACCATCTCTCTCTTCT 22
1 CGCACCATCTCTCTCTTCT 21

Db 1 CGCACCATCTCTCTCTTCT 21

RESULT 4
LOCUS AX146648 21 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 2 from Patent WO0134093.
ACCESSION AX146648
VERSION AX146648.1 GI:14285041
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
COMMENT other sequences; artificial sequences.

AUTHORS Agrawal, S.
TITLE Potentiation of prodrug efficacy
JOURNAL Patent: WO 0134093-A 2 17-MAY-2001;
HYBRIDON, INC. (US)

FEATURES Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide sequence"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTCT 21
1 TCGACCCATCTCTCTCTTCT 21

Db 1 TCGACCCATCTCTCTCTTCT 21

RESULT 5
LOCUS AX203700 21 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 35 from Patent WO0152904.
ACCESSION AX203700
VERSION AX203700.1 GI:15393146
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Gill, P.S. and Masood, R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 35 26-JUL-2001;
Gill, Parkash, S. (US)
FEATURES Location/Qualifiers
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Scrambled mixed backbone oligonucleotides, nucleotides 1-4 and 18-21 and 2' O methylribonucleosides"

ORIGIN

Query Match 95.5%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTCT 21
1 TCGACCCATCTCTCTCTTCT 21

Db 1 TCGACCCATCTCTCTCTTCT 21

RESULT 6
LOCUS BD077063 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel HIV-specific synthetic oligonucleotide and method of using the same.
ACCESSION BD077063
VERSION BD077063.1 GI:22622666
KEYWORDS JP 2001514884-A/1.
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
REFERENCE 1 (bases 1 to 21)
AUTHORS Agrawal, S.
TITLE Novel HIV-specific synthetic oligonucleotide and method of using the same
JOURNAL Patent: JP 2001514884-A 1 18-SEP-2001;
HYBRIDON INC
COMMENT OS Human immunodeficiency virus

Qy	1 TCGCACCATCTCTCCTTC 21
Db	1 TCGCACCCATCTCTCCTTC 21

PN JP 2001514884-A/4
 PD 18-SEP-2001
 PF 05-AUG-1998 JP 2000509820
 PR 19-AUG-1997 US 08/914827
 PI SUDHIR AGRAWAL
 PC C12N15/09, A61K31/7125, A61P31/18, C12N15/00
 CC Novel HIV-specific synthetic oligonucleotide and method of
 using the same

FEATURES
source
FH Key Location/Qualifiers
FT source 1..21
/organism="Human immunodeficiency virus".
Location/Qualifiers
1..21
/organism="Human immunodeficiency virus"
/mol_type="genomic DNA"
/db_xref="taxon:12721"

ORIGIN
Query Match 95.5%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGACCCATCTCTCTCTCT 22
|||||
1 CGACCCATCTCTCTCTCT 21

Db 1 CGACCCATCTCTCTCTCT 21

RESULT 10
BD077068 21 bp DNA linear PAT 27-AUG-2002
LOCUS Novel HIV-specific synthetic oligonucleotide and method of using
DEFINITION the same.
ACCESSION BD077068
VERSION BD077068.1 GI:22622671
KEYWORDS JP 2001514884-A/6.
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
Virusae; Retroviridae; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 21)
Agrawal,S.
Novel HIV-specific synthetic oligonucleotide and method of using
the same.
Patent: JP 2001514884-A 6 18-SEP-2001;
JOURNAL HYBRIDON INC
COMMENT OS Human immunodeficiency virus
PN JP 2001514884-A/6
PD 18-SEP-2001
PF 05-AUG-1998 JP 2000509820
PR 19-AUG-1997 US 08/914827
PI SUDHIR AGRAWAL
PC C12N15/09,A61K31/7125,A61P31/18,C12N15/00
CC Novel HIV-specific synthetic oligonucleotide and method of CC
using the same

FEATURES
source
FH Key Location/Qualifiers
FT source 1..21
/organism="Human immunodeficiency virus".
Location/Qualifiers
1..21
/organism="Human immunodeficiency virus"
/mol_type="genomic DNA"
/db_xref="taxon:12721"

ORIGIN
Query Match 95.5%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGACCCATCTCTCTCTC 21
|||||
1 TCGACCCATCTCTCTCTC 21

Db 1 TCGACCCATCTCTCTCTC 21

RESULT 11
I49134 20 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 8 from patent US 5627277.
DEFINITION I49134
ACCESSION I49134
VERSION I49134.1 GI:2467597
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
1 (bases 1 to 20)
REFERENCE Cohen,A.S., Bourque,A. and Vilenchik,M.
AUTHORS Method for analyzing oligonucleotide analogs
TITLE Patent: US 5627277-A 8 06-MAY-1997;
JOURNAL Location/Qualifiers
FEATURES 1..20
source /organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 90.9%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCACCCATCTCTCTCTCT 22
|||||
1 GCACCCATCTCTCTCTCT 20

Db 1 GCACCCATCTCTCTCTCT 20

RESULT 12
AR206325 21 bp DNA linear PAT 20-JUN-2002
LOCUS AR206325
DEFINITION Sequence 5 from patent US 6372427.
ACCESSION AR206325
VERSION AR206325.1 GI:21504894
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 21)
Kandimala,E.R. and Agrawal,S.
Cooperative oligonucleotides
Patent: US 6372427-A 5 16-APR-2002;
JOURNAL Location/Qualifiers
FEATURES 1..21
source /organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 90.9%; Score 20; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGACCCATCTCTCTCTT 20
|||||
2 TCGACCCATCTCTCTCTT 21

Db 2 TCGACCCATCTCTCTCTT 21

RESULT 13
AR374987 21 bp mRNA linear PAT 18-DEC-2003
LOCUS AR374987
DEFINITION Sequence 1 from patent US 6605708.
ACCESSION AR374987
VERSION AR374987.1 GI:40078169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 21)
Habus,I. and Agrawal,S.
Building blocks with carbamate internucleoside linkages and
oligonucleotides derived therefrom
Patent: US 6605708-A 1 12-AUG-2003;
JOURNAL Location/Qualifiers
FEATURES 1..21
source /organism="unknown"
/mol_type="mRNA"

ORIGIN
Query Match 90.9%; Score 20; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 45;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGACCCATCTCTCTCTT 20
 |||||

Db 2 TCGACCCATCTCTCTCTT 21
 |||||

RESULT 14

ARI70398

LOCUS ARI70398 22 bp DNA linear PAT 17-DEC-2001
 DEFINITION Sequence 24 from patent US 6291438.

ACCESSION ARI70398

VERSION ARI70398.1 GI:17908357

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 22)

AUTHORS Wang, J.H.

TITLE Antiviral anticancer poly-substituted phenyl derivatized

oligoribonucleotides and methods for their use

JOURNAL Patent: US 6291438-A 24 18-SEP-2001;

FEATURES Location/Qualifiers

1..22

source /organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 90.9%; Score 20; DB 6; Length 22;

Best Local Similarity 100.0%; Pred. No. 45;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCACCATCTCTCTCTT 22
 |||||

Db 2 GCACCATCTCTCTCTT 21
 |||||

RESULT 15

ARI40320/c

LOCUS ARI40320 22 bp DNA linear PAT 16-JUN-2001
 DEFINITION Sequence 8 from patent US 6207455.

ACCESSION ARI40320

VERSION ARI40320.1 GI:14482816

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 22)

AUTHORS Chang, L.-J.

TITLE Lentiviral vectors

JOURNAL Patent: US 6207455-A 8 27-MAR-2001;

FEATURES Location/Qualifiers

1..22

source /organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 88.2%; Score 19.4; DB 6; Length 22;

Best Local Similarity 95.2%; Pred. No. 90;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGACCCATCTCTCTCTT 21
 |||||

Db 21 TCGACCCATCTCTCTCTT 1
 |||||

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 Job time : 809.372 secs

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OM nucleic - nucleic search, using sw model

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Title: US-09-896-692B-5

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	22	2	AAx19779 Human imm
2	21	95.5	21	2	AAx19783 Human imm
3	21	95.5	21	2	AAx19784 Human imm
4	21	95.5	21	2	AAx19781 Human imm
5	21	95.5	21	2	AAx19782 Human imm
6	21	95.5	21	2	AAx19780 Human imm
7	21	95.5	21	4	AAH21706 HIV-1 gag
8	21	95.5	21	4	AAH23028 Control m
9	21	95.5	21	8	ACC59011 Human Gag
10	21	95.5	21	10	ADC24663 Antisense
11	21	95.5	21	10	ABX90517 Mixed bac
12	20	90.9	21	2	AAx1968 HIV-1 gag
13	20	90.9	21	2	AAx1968 HIV-1 gag
14	20	90.9	21	2	AAx1968 HIV-1 gag
15	20	90.9	21	9	ADA18562 Cooperati
16	20	90.9	22	6	AD22554 Human imm
17	19.4	88.2	22	2	AAx1969 HIV-1 gag
18	19.4	88.2	22	2	AAx1969 HIV-1 gag
19	19.4	88.2	22	3	AAZ88083 Vector PT
20	19.4	88.2	22	5	AAf55618 HIV-1 vec

21	19.4	88.2	22	9	ADA18563 Cooperati
C 22	19	86.4	19	10	ADG35586 HIV gINA
C 23	19	86.4	19	10	ADG35597 HIV gINA
C 24	19	86.4	19	10	ADG35577 HIV gINA
C 25	19	86.4	19	10	ADG36324 HIV gINA
C 26	19	86.4	19	10	ADG36315 HIV gINA
C 27	19	86.4	19	10	ADG35623 HIV gINA
C 28	19	86.4	19	10	ADG36325 HIV gINA
C 29	19	86.4	19	10	ADG36361 HIV gINA
C 30	19	86.4	20	2	AAQ43467 HIV viral
C 31	19	86.4	20	2	AAQ61815 Antisense
C 32	19	86.4	20	2	AAx10969 HIV gag c
C 33	19	86.4	20	2	AAV28224 Antisense
C 34	19	86.4	20	2	AAx18753 Target HI
C 35	19	86.4	20	2	AAx23632 Deletion
C 36	19	86.4	22	6	AAx32576 Antisense
C 37	19	86.4	22	6	AAx32585 Antisense
C 38	19	86.4	22	6	AAx32579 Antisense
C 39	19	86.4	22	6	AAx32578 Antisense
C 40	19	86.4	22	6	AAx32575 Antisense
C 41	19	86.4	22	6	AAx32573 Antisense
C 42	19	86.4	22	6	AAx32580 Antisense
C 43	19	86.4	22	6	AAx32581 Antisense
C 44	19	86.4	22	6	AAx32583 Antisense
C 45	19	86.4	22	6	AAx32574 Antisense

ALIGNMENTS

RESULT 1
AAx19779 standard; DNA; 22 BP.
ID AAX19779;
AC AAX19779;
XX 08-UN-1999 (first entry)
XX Human immunodeficiency virus antisense oligonucleotide SEQ ID NO:5.
XX Human immunodeficiency virus; HIV; phosphorothioate linkage; gag;
XX infection; antisense oligonucleotide; ss.
XX
XX Synthetic.
XX Human immunodeficiency virus 1.
OS
OS
FH Key location/Qualifiers
FT modified_base 1..22
FT /tag= a
FT /note= "phosphorothioate linkages"
PN
PN W09909154-A2.
PD 25-FEB-1999.
XX
XX 05-AUG-1998; 98WO-US016345.
XX
XX 19-AUG-1997; 97US-00914827.
XX
XX (HYBR-) HYBRIDON INC.
XX
XX Agrawal S;
XX WPI, 1999-228890/19.
XX
XX New synthetic oligonucleotide sequences antisense to conserved gag region
XX of HIV-1 genome.
XX
XX Claim 1; Page 64; 64pp; English.
XX
XX The present sequence represents a synthetic oligonucleotide sequence,
XX antisense to a conserved gag region of the HIV-1 genome. The antisense
XX oligonucleotide can be used to treat HIV-1 or HIV-2 infection in a

CC mammal, or inhibit HIV-1 or HIV-2 in a cell. The oligonucleotide has less
CC cell toxicity, provokes less immunostimulus than prior art, and is a GC-
CC rich antisense HIV oligonucleotide
XX
SQ Sequence 22 BP; 2 A; 11 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTCT 22
DB 1 TCGACCCATCTCTCTCTCT 22

RESULT 2

AAK19783
ID AAK19783 standard; DNA; 21 BP.

AAK19783;

08-JUN-1999 (first entry)

Human immunodeficiency virus antisense oligonucleotide SEQ ID NO:4.

Human immunodeficiency virus; HIV; phosphorothioate linkage; gag;
infection; antisense oligonucleotide; ss.

Synthetic.

Human immunodeficiency virus 1.

Key Location/Qualifiers
modified_base 1..21
FT a
FT /note= "phosphorothioate linkages"

W09909154-A2.

25-FEB-1999.

05-AUG-1998; 98WO-US016345.

19-AUG-1997; 97US-00914827.

(HYBR-) HYBRIDON INC.

Agrawal S;

WPI; 1999-228690/19.

New synthetic oligonucleotide sequences antisense to conserved gag region
of HIV-1 genome.

Claim 13; Page 63; 64pp; English.

The present sequence represents a synthetic oligonucleotide sequence,
antisense to a conserved gag region of the HIV-1 genome. The antisense
oligonucleotide can be used to treat HIV-1 or HIV-2 infection in a
mammal, or inhibit HIV-1 or HIV-2 in a cell. The oligonucleotide has less
cell toxicity, provokes less immunostimulus than prior art, and is a GC-
rich antisense HIV oligonucleotide

Sequence 21 BP; 2 A; 11 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGACCCATCTCTCTCTCT 22
DB 1 CGACCCATCTCTCTCTCT 21

RESULT 3
AAK19784
ID AAK19784 standard; DNA; 21 BP.

AAK19784;

08-JUN-1999 (first entry)

Human immunodeficiency virus antisense oligonucleotide SEQ ID NO:6.

Human immunodeficiency virus; HIV; phosphorothioate linkage; gag;
infection; antisense oligonucleotide; ss.

Synthetic.

Human immunodeficiency virus 1.

Key Location/Qualifiers
modified_base 1..21
FT a
FT /note= "phosphorothioate linkages"

W09909154-A2.

25-FEB-1999.

05-AUG-1998; 98WO-US016345.

19-AUG-1997; 97US-00914827.

(HYBR-) HYBRIDON INC.

Agrawal S;

WPI; 1999-228690/19.

New synthetic oligonucleotide sequences antisense to conserved gag region
of HIV-1 genome.

Claim 28; Page 64; 64pp; English.

The present sequence represents a synthetic oligonucleotide sequence,
antisense to a conserved gag region of the HIV-1 genome. The antisense
oligonucleotide can be used to treat HIV-1 or HIV-2 infection in a
mammal, or inhibit HIV-1 or HIV-2 in a cell. The oligonucleotide has less
cell toxicity, provokes less immunostimulus than prior art, and is a GC-
rich antisense HIV oligonucleotide

Sequence 21 BP; 2 A; 11 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTC 21
DB 1 TCGACCCATCTCTCTCTTC 21

RESULT 4

AAK19781
ID AAK19781 standard; DNA; 21 BP.

AAK19781;

08-JUN-1999 (first entry)

Human immunodeficiency virus antisense oligonucleotide SEQ ID NO:3.

Human immunodeficiency virus; HIV; phosphorothioate linkage; gag;
infection; antisense oligonucleotide; ss.

Synthetic.

Human immunodeficiency virus 1.

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XX Key Location/Qualifiers
FH modified_base 1..21
FT /*tag= a
FT /note= "phosphorothioate linkages"
XX
XX WO9909154-A2.
XX
XX 25-FEB-1999.
XX
XX 05-AUG-1998; 98WO-US016345.
XX
XX 19-AUG-1997; 97US-00914827.
XX
XX (HYBR-) HYBRIDON INC.
XX
XX Agrawal S;
XX
XX WPI; 1999-228890/19.
XX
XX New synthetic oligonucleotide sequences antisense to conserved gag region
XX of HIV-1 genome.
XX
XX Claim 9; Page 63; 64pp; English.
XX
XX The present sequence represents a synthetic oligonucleotide sequence,
XX antisense to a conserved gag region of the HIV-1 genome. The antisense
XX oligonucleotide can be used to treat HIV-1 or HIV-2 infection in a
XX mammal, or inhibit HIV-1 or HIV-2 in a cell. The oligonucleotide has less
XX cell toxicity, provokes less immunostimulus than prior art, and is a GC-
XX rich antisense HIV oligonucleotide
XX
XX Sequence 21 BP; 2 A; 11 C; 1 G; 4 T; 3 U; 0 Other;
SQ
XX
XX Query Match 95.5%; Score 21; DB 2; Length 21;
XX Best Local Similarity 85.7%; Pred. No. 17;
XX Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY
XX 2 CGACCCCATCTCTCTCTCT 22
XX |||||
XX 1 CGACCCCATCTCTCTCTCU 21
DB
XX
XX RESULT 5
XX AAX19782
XX ID AAX19782 standard; DNA; 21 BP.
XX
XX AAX19782;
XX
XX 08-JUN-1999 (first entry)
XX
XX Human immunodeficiency virus antisense oligonucleotide SEQ ID NO:2.
XX
XX Human immunodeficiency virus; HIV; phosphorothioate linkage; gag;
XX infection; antisense oligonucleotide; ss.
XX
XX Synthetic.
XX
XX Human immunodeficiency virus 1.
XX
XX Key Location/Qualifiers
XX modified_base 1..21
XX /*tag= a
XX /note= "phosphorothioate linkages"
XX
XX WO9909154-A2.
XX
XX 25-FEB-1999.
XX
XX 05-AUG-1998; 98WO-US016345.
XX
XX 19-AUG-1997; 97US-00914827.
XX
XX (HYBR-) HYBRIDON INC.
XX
XX
XX

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```

XX Agrawal S;
XX
XX WPI; 1999-228890/19.
XX
XX New synthetic oligonucleotide sequences antisense to conserved gag region
XX of HIV-1 genome.
XX
XX Claim 12; Page 63; 64pp; English.
XX
XX The present sequence represents a synthetic oligonucleotide sequence,
XX antisense to a conserved gag region of the HIV-1 genome. The antisense
XX oligonucleotide can be used to treat HIV-1 or HIV-2 infection in a
XX mammal, or inhibit HIV-1 or HIV-2 in a cell. The oligonucleotide has less
XX cell toxicity, provokes less immunostimulus than prior art, and is a GC-
XX rich antisense HIV oligonucleotide
XX
XX Sequence 21 BP; 2 A; 11 C; 1 G; 7 T; 0 U; 0 Other;
SQ
XX
XX Query Match 95.5%; Score 21; DB 2; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
XX 1 TCGACCCCATCTCTCTCTC 21
XX |||||
XX 1 TCGACCCCATCTCTCTCTC 21
DB
XX
XX RESULT 6
XX AAX19780
XX ID AAX19780 standard; DNA; 21 BP.
XX
XX AAX19780;
XX
XX 08-JUN-1999 (first entry)
XX
XX Human immunodeficiency virus antisense oligonucleotide SEQ ID NO:1.
XX
XX Human immunodeficiency virus; HIV; phosphorothioate linkage; gag;
XX infection; antisense oligonucleotide; ss.
XX
XX Synthetic.
XX
XX Human immunodeficiency virus 1.
XX
XX Key Location/Qualifiers
XX modified_base 1..21
XX /*tag= a
XX /note= "phosphorothioate linkages"
XX
XX WO9909154-A2.
XX
XX 25-FEB-1999.
XX
XX 05-AUG-1998; 98WO-US016345.
XX
XX 19-AUG-1997; 97US-00914827.
XX
XX (HYBR-) HYBRIDON INC.
XX
XX Agrawal S;
XX
XX WPI; 1999-228890/19.
XX
XX New synthetic oligonucleotide sequences antisense to conserved gag region
XX of HIV-1 genome.
XX
XX Claim 8; Page 63; 64pp; English.
XX
XX The present sequence represents a synthetic oligonucleotide sequence,
XX antisense to a conserved gag region of the HIV-1 genome. The antisense
XX oligonucleotide can be used to treat HIV-1 or HIV-2 infection in a
XX mammal, or inhibit HIV-1 or HIV-2 in a cell. The oligonucleotide has less
XX cell toxicity, provokes less immunostimulus than prior art, and is a GC-
XX

```

CC rich antisense HIV oligonucleotide
 XX
 SQ Sequence 21 BP; 2 A; 11 C; 1 G; 4 T; 3 U; 0 Other;
 Query Match 95.5%; Score 21; DB 2; Length 21;
 Best Local Similarity 85.7%; Pred. No. 17;
 Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTC 21
 :|||||
 DB 1 UCGACCCATCTCTCTCTTC 21

RESULT 7
 ID AAH21706 standard; DNA; 21 BP.
 AC AAH21706;
 DT 11-SEP-2003 (revised)
 DT 13-AUG-2001 (first entry)
 XX
 DE HIV-1 gag gene phosphorothioate oligonucleotide.
 XX
 KW Phosphorothioate; MDM-2; HIV-1; gag; pancreatic cancer; tumour;
 KW Panc 1 tumour; colon cancer; prodrug; polyanion; ss.
 XX
 OS Human immunodeficiency virus 1.
 PH Key Location/Qualifiers
 FT modified_base 1..21
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages"
 FT misc_RNA 1..2
 FT /tag= b
 FT /note= "2'-O-methylribonucleosides"
 FT misc_RNA 18..21
 FT /tag= c
 FT /note= "2'-O-methylribonucleosides"
 XX
 PN WO200134093-A2.
 XX
 PD 17-MAY-2001.
 XX
 PF 08-NOV-2000; 2000WO-US030687.
 XX
 PR 09-NOV-1999; 99US-0164182P.
 XX
 PA (HYBR-) HYBRIDON INC.
 XX
 PI Agrawal S;
 XX
 DR WPI; 2001-300586/31.
 XX
 PT Potentiating prodrug activity, without producing side effects, involves
 PT co-administering a prodrug with a polyanion.
 XX
 PS Example 1; Page 12; 26pp; English.

CC The present invention describes a method for potentiating prodrug
 CC activity, without producing side effects, comprising co-administering the
 CC prodrug with a polyanion which is not an oligonucleotide having two 5',
 CC and four 3'2'-O-methylribonucleosides with the sequence: 5'-
 CC UGACCTGTCTACUCAC-3'. Also described are: (1) potentiating the activity
 CC of a prodrug without producing side effects, comprising administering a
 CC polyanion before the prodrug; and (2) potentiating the activity of a
 CC polyanion without producing side effects, comprising co-administering a
 CC polyanion and a prodrug in a dosage which would not produce a therapeutic
 CC effect in the absence of the polyanion. The methods can be used for
 CC potentiating prodrug activity without producing side effects. The
 CC potentiating agents maximize the efficacy of the prodrugs, reducing the
 CC dosage to be administered to less toxic levels. The present sequence

CC represents a phosphorothioate oligonucleotide complementary to HIV-1 gag,
 CC which is used in an example from the present invention for the treatment
 CC of colon cancer tumour-bearing mice. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 21 BP; 2 A; 11 C; 1 G; 4 T; 3 U; 0 Other;
 Query Match 95.5%; Score 21; DB 4; Length 21;
 Best Local Similarity 85.7%; Pred. No. 17;
 Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTC 21
 :|||||
 DB 1 UCGACCCATCTCTCTCTTC 21

RESULT 8
 ID AAH23028 standard; DNA; 21 BP.
 AC AAH23028;
 DT 17-SEP-2001 (first entry)
 XX
 DE Control mixed backbone scrambled oligonucleotide.
 XX
 KW Vascular endothelial growth factor; VEGF; antisense; angiogenesis;
 KW cell proliferation; Kaposi's sarcoma; cancer; melanoma; cytostatic;
 KW antisense therapy; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN WO200152904-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 19-JAN-2001; 2001WO-US000019.
 XX
 PR 19-JAN-2000; 2000US-00487023.
 XX
 PA (GILL/) GILL P S.
 XX
 PI Gill PS, Masood R;
 XX
 DR WPI; 2001-451896/48.
 XX
 PT Novel antisense oligonucleotides useful for inhibiting vascular
 PT endothelial growth factor expression, angiogenesis and for treating
 PT cancer, e.g., Kaposi's sarcoma, ovarian cancer and prostate cancer.
 XX
 PS Example 13; Page 57; 105pp; English.

CC The invention provides a composition comprising one or more antisense
 CC oligonucleotides directed against vascular endothelial growth factor
 CC (VEGF) where the antisense oligonucleotides inhibits proliferation of
 CC cells exhibiting autocrine VEGF activity at an IC 50 concentration of
 CC between 0.5-2.5 micro M. The antisense oligonucleotides may be directed
 CC against VEGF for inhibiting cancer cell proliferation and angiogenesis.
 CC Preferably the oligonucleotide AAH23032 (a modified version of AAH2984)
 CC is used and may be utilized to treat Kaposi's sarcoma, ovarian cancer,
 CC prostate cancer, pancreatic cancer or melanoma. The present sequence
 CC represents a control mixed backbone scrambled oligonucleotide

SQ Sequence 21 BP; 2 A; 11 C; 1 G; 4 T; 3 U; 0 Other;
 Query Match 95.5%; Score 21; DB 4; Length 21;
 Best Local Similarity 85.7%; Pred. No. 17;
 Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTC 21
 :|||||
 DB 1 UCGACCCATCTCTCTCTTC 21

RESULT 9
ACCS9011
ID ACCS9011 standard; DNA; 21 BP.
XX
AC ACCS9011;
XX
DT 01-JUL-2003 (first entry)
XX
DE Human Gag/HIV-1 antisense oligonucleotide.
XX
XX Human; antisense; transcobalamin receptor; intrinsic factor receptor;
XX cytosolic; antiviral; anti-HIV; hepatotropic; antiinflammatory;
XX virocidic; tuberculostatic; protozoacide; cancer; viral disease; ss; Gag;
XX HIV-1.
XX
OS Homo sapiens.
XX
PN WO2003025139-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-US029571.
XX
PR 17-SEP-2001; 2001US-0322821P.
XX
PR 13-SEP-2002; 2002US-0410627P.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI Collins DA, Callstrom M, Prendergast FG;
XX
XX WPI; 2003-430085/40.
XX
DR Compound useful for treating e.g. cancer comprises optionally stabilized
XX nucleic acid, aptamer, antisense sequence, or antisense mimic conjugated
XX to a ligand for the transcobalamin receptor or intrinsic factor receptor.
XX
PS Disclosure; Page 88; 156pp; English.
XX
XX The invention relates to a novel compound comprising an optionally
XX stabilised nucleic acid or its analogue encoding a peptide, protein or
XX other biological modifier, aptamer, antisense sequence, or antisense
XX mimic conjugated directly or through a linker to a ligand for the
XX transcobalamin receptor or intrinsic factor receptor. A compound of the
XX invention has cytosolic, antiviral, anti-HIV, hepatotropic,
XX antiinflammatory, virucide, tuberculostatic, and protozoacide activity.
XX The compounds may be useful in the manufacture of a medicament for the
XX delivery of material that affects gene translation or gene transcription
XX and modulates a biological process, in medical therapy. A compound is
XX also useful for treating cancer, viral diseases such as infection caused
XX by HIV, hepatitis (hepatitis B, hepatitis C and hepatitis D), herpes, TB,
XX Epstein-Barr virus, malaria, influenza virus, Para influenza virus, mumps
XX virus, adenoviruses, reoviruses, respiratory syncytial virus,
XX rhinoviruses, polioviruses, coxsackie-viruses, echoviruses,
XX enteroviruses, gastroenteritis viruses, rubella viruses, rubella virus,
XX molluscum contagiosum virus, human parvovirus B19, cytomegalovirus, human
XX papillomavirus, varicella zoster, arenaviruses or filoviruses. The
XX present sequence is used in the exemplification of the invention
XX
SQ Sequence 21 BP; 2 A; 11 C; 1 G; 4 T; 3 U; 0 Other;

Query Match 95.5%; Score 21; DB 8; Length 21;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 TCGACCCATCTCTCTCTC 21
:|||||||:|:|
1 UCGACCCATCTCTCTCUC 21

RESULT 10
ADC24663

ID ADC24663 standard; DNA; 21 BP.
XX
AC ADC24663;
XX
XX
DT 18-DEC-2003 (first entry)
XX
DE Antisense DNA #11 that can be conjugated to the carriers of invention.
XX
XX cobalamin-bound detectable; radioimaging; infectious disease;
XX cardiovascular disorder; antibiotic; antiviral agent; ss.
XX
OS Synthetic.
XX
PN WO2003026674-A1.
XX
PD 03-APR-2003.
XX
PF 30-SEP-2002; 2002WO-US031038.
XX
PR 28-SEP-2001; 2001US-0326183P.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
PI Collins DA;
XX
XX WPI; 2003-393314/37.
XX
DR Composition useful for the treatment of e.g. infectious disease,
XX comprises a cobalamin-bound detectable or therapeutic agent in
XX combination with a cobalamin transport protein.
XX
PS Example 4; SEQ ID NO 11; 97pp; English.
XX
XX The present invention relates to a cobalamin-bound detectable or
XX therapeutic agent in combination with a cobalamin transport protein. In
XX the manufacture of a medicament to increase the uptake of detectable
XX agent useful in radioimaging or therapeutic agent for treatment of a
XX disorder associated with abnormal cellular proliferation, an infectious
XX disease and cardiovascular disorder, as an antibiotic or antiviral agent;
XX for transcription of a factor. The method increases efficiency of
XX vitamin B12 or vitamin B12 conjugated materials. The presents sequence
XX represents an antisense nucleotide that can be conjugated to the carriers
XX described in the present invention.
XX
SQ Sequence 21 BP; 2 A; 11 C; 1 G; 4 T; 3 U; 0 Other;

Query Match 95.5%; Score 21; DB 10; Length 21;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

1 TCGACCCATCTCTCTCTC 21
:|||||||:|:|
1 UCGACCCATCTCTCTCUC 21

RESULT 11
ABX90517
ID ABX90517 standard; DNA; 21 BP.
XX
AC ABX90517;
XX
DT 01-MAY-2003 (first entry)
XX
DE Mixed backbone scrambled control antisense oligonucleotide.
XX
XX Antisense; ss; probe; VEGF; vascular endothelial growth factor; cancer;
XX angiogenesis; neoplastic proliferation; cellular proliferation.
XX
OS Synthetic.
XX
PN US2002165174-A1.
XX
PD 07-NOV-2002.

XX 13-MAR-2001; 2001US-00805761.
XX
XX 31-JAN-1997; 97US-0037004P.
PR 30-JAN-1998; 98US-00016541.
PR 19-JAN-2000; 2000US-00487023.
PR 19-JAN-2001; 2001WO-US000019.
XX
XX (GILL/) GILL P S.
PA (MASO/) MASOOD R.
XX
XX Gill PS, Masood R;
XX
XX WPI; 2003-255224/25.
XX
XX New composition comprising an antisense oligonucleotide directed against
PT vascular endothelial growth factor, useful for preparing a composition
PT for treating cancer.
XX
XX Example 13; Page 20; 54pp; English.
XX
XX The invention relates to a composition comprising an antisense
CC oligonucleotide directed against vascular endothelial growth factor
CC (VEGF). The antisense oligonucleotide is useful for preparing a
CC composition treating cancer, neoplastic proliferation, abnormal cellular
CC proliferation and preventing angiogenesis. The present sequence is a
CC scrambled control antisense oligonucleotide
XX
XX Sequence 21 BP; 2 A; 11 C; 1 G; 4 T; 3 U; 0 Other;
SQ

Query Match 95.5%; Score 21; DB 10; Length 21;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCCTTC 21
:|||||
1 UCGACCCATCTCTCTCCTTC 21

Db 1 UCGACCCATCTCTCTCCTTC 21

RESULT 12
AAT46110
ID AAT46110 standard; DNA; 21 BP.
XX
XX AAT46110;
AC
XX
XX 25-FEB-1997 (first entry)
DT
XX
XX Oligo 1 contg. carbamate internucleoside linkage.
DE
XX
XX carbamate; internucleoside; linkage; phosphodiester; phosphorothioate;
KW nuclease resistant; stable; stable duplex formation; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..21
FT /tag= a
FT /note= "phosphodiester backbone"
FT modified_base 20..21
FT /tag= b
FT /note= "3'-NH-COO-5' (carbamate) linkage"
PN WO9504066-A1.
XX
XX 09-FEB-1995.
PD
XX
XX 27-JUL-1994; 94WO-US008655.
PF
XX
XX 28-JUL-1993; 93US-00098945.
PR
XX
XX (HYBR-) HYBRIDON INC.
PA
XX
XX Habus I, Agrawal S;
PI

XX WPI, 1995-082177/11.
XX
XX New oligo:nucleotide building blocks - comprising a di:nucleoside
PT carbamate to form prods. with nuclease resistance and stable duplex
PT formation.
XX
XX Example 2; Page 18; 38pp; English.
XX
XX AAT46110-16 are oligonucleotides (ON) contg. novel carbamate inter-
CC nucleoside linkages. Dinucleoside carbamates having the structure 5'-
CC nucleoside-3'-NHCOO-5'-nucleoside-3' are claimed as building blocks for
CC ON synthesis. The carbamate internucleoside linkages provide increased
CC resistance to nucleolytic degradation without hindering the ability of
CC the ONs to undergo base stacking, and in prefcd. configurations, without
CC destabilising the double helix formed between the ONs and their
CC complementary target nucleic acids
XX
XX Sequence 21 BP; 2 A; 11 C; 1 G; 7 T; 0 U; 0 Other;
SQ

Query Match 90.9%; Score 20; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCCTT 20
:|||||
2 TCGACCCATCTCTCTCCTT 21

Db 2 TCGACCCATCTCTCTCCTT 21

RESULT 13
AAT41968
ID AAT41968 standard; CDNA; 21 BP.
XX
XX AAT41968;
AC
XX
XX 24-JUN-1997 (first entry)
DT
XX
XX HIV-1 gag binding oligonucleotide used as antisense HIV inhibitor.
DE
XX
XX Co-operative binding; duplex; antisense inhibition; target sequence;
KW human immunodeficiency virus; HIV; dimerisation domain; T structure;
KW gene function; ss.
XX
XX Synthetic.
OS
XX
XX WO9632474-A1.
PN
XX
XX 17-OCT-1996.
PD
XX
XX 04-APR-1996; 96WO-US004605.
PF
XX
XX 12-APR-1995; 95US-00420672.
PR
XX
XX (HYBR-) HYBRIDON INC.
PA
XX
XX Kandimala ER, Agrawal S;
PI
XX
XX WPI, 1996-477125/47.
DR
XX
XX Compn. contg. at least two co-operative oligo:nucleotide(s)
PT complementary to a target sequence - and with mutually complementary
PT dimerisation domains, for use as antisense inhibitors of HIV and
PT influenza virus.
XX
XX Disclosure; Page 43; 84pp; English.
PS
XX
XX AAT41965-T41994 are oligonucleotides (ON) that bind to HIV-1 mRNA and/or
CC DNA and act as antisense inhibitors of HIV-1 gene expression. The ON are
CC preferably used as duplexes, i.e. a first ON has a region that binds to
CC an HIV-1 target sequence in a 5'-3' direction and a second region
CC complementary to a second ON which has a first region which binds to the
CC same target HIV-1 sequence but in a 3'-5' direction and a second region
CC complementary to the first ON. Both ON bind to the HIV target sequence up

CC until a certain point along the target sequence, where the two binding ON
CC are in close proximity and the remainder of the binding ON bind each
CC other. AAT94859-141971 lack a dimerisation domain (domain hybridising to
CC a second antisense ON) but these may be added to give extra stability to
CC the inhibiting complex. The duplex/target site complex forms a T-shaped
CC structure, inhibiting expression of HIV-1 nucleic acid. Also co-operative
CC ON, when labelled, can be used to identify specific bacteria or viruses
CC in cell cultures; to study function of specific genes as an alternative
CC to use of 'knock out' animals. Co-operative ON have improved affinity and
CC sequence specificity, reduced toxicity and better antisense activity
CC compared with single, longer ON. Insertion of dimerisation domains into
CC antisense ON provides a more stable complex

CC Sequence 21 BP; 2 A; 11 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 90.9%; Score 20; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGACCCATCTCTCTCTT 20
Db 2 TCGACCCATCTCTCTCTT 21

RESULT 14

AAT94859
ID AAT94859 standard; cDNA; 21 BP.

AC AAT94859;

DT 22-APR-1998 (first entry)

DE HIV-1 gag gene antisense oligonucleotide.

KW gag gene; initiation codon region; target region; dimerisation domain;

KM synthetic cooperative oligonucleotide; affinity; specificity; ss.

KW antisense molecule; treatment; viral infection; influenza; HIV; ss.

OS Synthetic.

PN WO9738097-A1.

PD 16-OCT-1997.

PF 04-APR-1997; 97WO-US005683.

PR 04-APR-1996; 96US-00627967.

PA (HYBR-) HYBRIDON INC.

PI Kandimala ER, Agrawal S;

DR WPI; 1997-512714/47.

PT Anti-sense oligo:nucleotide compositions have at least 2 cooperative
PT oligo:nucleotide(s) having a targeting and a dimerisation region -
PT useful for inhibition of target nucleic acid expression.

PS Disclosure; Page 17; 91pp; English.

CC The present oligonucleotide is an antisense oligonucleotide that binds to
CC part of the gag gene of Human immunodeficiency virus type 1 (HIV-1)
CC (AAT94853-54 and AAT94866). The oligonucleotide is used to exemplify the
CC method of the invention. This method comprises two synthetic cooperative
CC oligonucleotides, where each oligonucleotide comprises a region
CC complementary to one of tandem, non-overlapping regions of a target
CC nucleic acid, and a dimerisation domain at a terminus of each of the
CC oligonucleotides. The dimerisation domains of the oligonucleotides are
CC complementary to each other. The target nucleic acid is an mRNA, a single
CC -stranded viral DNA, or a single-stranded viral RNA. The synthetic
CC oligonucleotides can interact cooperatively to provide improved affinity,
CC specificity, and biological activity as antisense molecules. The

CC compositions are used for inhibiting the expression of target nucleic
CC acids. They can be used for the treatment of viral infections, e.g.
CC influenza (AAT94801-17) or HIV (AAT94853-92) infection. They can also be
CC used for the detection and study of target nucleic acids

CC Sequence 21 BP; 2 A; 11 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 90.9%; Score 20; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGACCCATCTCTCTCTT 20
Db 2 TCGACCCATCTCTCTCTT 21

RESULT 15

ADA18562
ID ADA18562 standard; DNA; 21 BP.

AC ADA18562;

DT 20-NOV-2003 (first entry)

DE Cooperative oligonucleotide #4.

KW Cooperative oligonucleotide; binding partner; cyclodextrin; adamantane;

KM streptavidin; pharmaceutical composition; nucleic acids expression; HIV;

KW acquired immunodeficiency syndrome; AIDS; anti-HIV; ss.

OS Synthetic.

PN US2003099959-A1.

PD 29-MAY-2003.

PF 22-JAN-2002; 2002US-00054429.

PR 12-APR-1995; 95US-00420672.

PA (KAND/) KANDIMALA E R.

PI (AGRA/) AGRAWAL S;

DR WPI; 2003-606628/57.

PT Oligonucleotide composition used to, e.g. treat mammal infected by human
PT immunodeficiency virus, comprises synthetic oligonucleotides linked to
PT binding partner consisting of cyclodextrin, adamantane, streptavidin, or
PT biotin.

PS Disclosure; Fig 6; 29pp; English.

CC The present invention relates to an oligonucleotide composition
CC comprising a first and second synthetic cooperative oligonucleotides
CC linked to their respective binding partner consisting of cyclodextrin,
CC adamantane, streptavidin, or biotin. Each oligonucleotide has a region
CC complementary to a tandem, non-overlapping region of a target nucleic
CC acid that is separated by 0-3 bases. The oligonucleotide composition is
CC useful as a pharmaceutical composition to inhibit the expression of
CC nucleic acids in vitro, or for treating a mammal infected by HIV or by
CC acquired immunodeficiency syndrome (AIDS). The cooperative
CC oligonucleotides have improved sequence specificity for a single-stranded
CC target, reduced toxicity, and improved biological activity as antisense
CC molecules. The present sequence represents a cooperative oligonucleotide
CC of the invention.

CC Sequence 21 BP; 2 A; 11 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 90.9%; Score 20; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	TCGACCCGATCTCTCCTT	20
Db	2	TCGACCCGATCTCTCCTT	21

Search completed: September 15, 2005, 00:56:59
Job time : 202.605 secs

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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 23:12:17; Search time 771.628 Seconds
(without alignments)
1318.718 Million cell updates/sec

Title: US-09-896-692B-4

Perfect score: 21

Sequence: 1 cgcaccatctctctctctct 21

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 952800

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

GenEmbl:*
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	6	I49133 Sequence 7
2	21	100.0	21	6	BD077065 Novel HIV
3	21	100.0	21	6	BD077066 Novel HIV
4	21	100.0	22	6	I49132 Sequence 6
5	21	100.0	22	6	BD077067 Novel HIV
6	20	95.2	21	6	I49134 Sequence 8
7	20	95.2	21	6	AX146648 Sequence
8	20	95.2	21	6	AX203700 Sequence
9	20	95.2	21	6	BD077063 Novel HIV
10	20	95.2	21	6	BD077064 Novel HIV
11	20	95.2	21	6	BD077068 Novel HIV
12	20	95.2	22	6	AR170398 Sequence
13	19	90.5	21	6	AR206325 Sequence
14	19	90.5	21	6	AR374987 Sequence
15	18.4	87.6	22	6	AR140320 Sequence
16	18.4	87.6	22	6	AR206326 Sequence
17	18.4	87.6	22	6	AR287299 Sequence
18	18	85.7	18	6	AX772003 Sequence
19	18	85.7	20	6	A27240 Antiviral D

20	18	85.7	20	6	BD192520 Composite
21	18	85.7	20	6	I09442 Sequence 6
22	18	85.7	20	6	I72636 Sequence 10
23	18	85.7	20	6	AR260544 Sequence
24	18	85.7	20	6	AR260545 Sequence
25	18	85.7	20	6	AR260561 Sequence
26	18	85.7	22	6	AR430157 Sequence
27	18	85.7	22	6	AR363503 Sequence
28	17.4	82.9	21	6	AR206343 Sequence
29	17	81.0	17	6	I28579 Sequence 32
30	17	81.0	17	6	I58741 Sequence 32
31	17	81.0	17	6	AR486969 Sequence
32	17	81.0	17	6	AR418589 Sequence
33	17	81.0	17	6	AX952328 Sequence
34	17	81.0	20	6	A45278 Sequence 9
35	17	81.0	20	6	AR055037 Sequence
36	17	81.0	20	6	AR116258 Sequence
37	17	81.0	20	6	AR156286 Sequence
38	15.8	75.2	21	6	AR206344 Sequence
39	15.4	73.3	20	6	AR100320 Sequence
40	15.4	73.3	20	6	AR149975 Sequence
41	15.4	73.3	20	6	BD227848 Antisense
42	15	71.4	19	6	I78667 Sequence 22
43	15	71.4	22	6	AX540488 Sequence
44	14.4	68.6	22	6	AR430542 Sequence
45	14.2	67.6	19	6	AR206333 Sequence

ALIGNMENTS

RESULT 1	I49133	21 bp	DNA	linear	PAT 07-OCT-1997
LOCUS	I49133	Sequence 7 from patent US 5627277.			
DEFINITION	I49133				
ACCESSION	I49133				
VERSION	I49133.1	GI:2467596			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 21)				
AUTHORS	Cohen, A.S., Bouque, A. and Vilenchik, M.				
TITLE	Method for analyzing oligonucleotide analogs				
JOURNAL	Patent: US 5627277-A 7 06-MAY-1997;				
FEATURES	Location/Qualifiers				
source	1..21				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	100.0%; Score 21; DB 6; Length 21;				
Best Local Similarity	100.0%; Pred. No. 7.6;				
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 CGCACCATCTCTCTCTCT 21				
DB	1 CGCACCATCTCTCTCTCT 21				
RESULT 2	BD077065	21 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD077065	Novel HIV-specific synthetic oligonucleotide and method of using the same.			
DEFINITION	BD077065				
ACCESSION	BD077065				
VERSION	BD077065.1	GI:22622668			
KEYWORDS	UP 2001514884-A/3.				
SOURCE	Human immunodeficiency virus				
ORGANISM	Human immunodeficiency virus				
REFERENCE	1 (bases 1 to 21)				

AUTHORS Agrawal, S.
TITLE Novel HIV-specific synthetic oligonucleotide and method of using the same
JOURNAL Patent: JP 2001514884-A 3 18-SEP-2001;
HYBRIDON INC

COMMENT OS Human immunodeficiency virus
PN JP 2001514884-A/3
PD 18-SEP-2001
PR 05-AUG-1998 JP 2000509820
PR 19-AUG-1997 US 08/914827
PI SUDHIR AGRAWAL
PC C12N15/09,A61K31/7125,A61P31/18,C12N15/00
CC Novel HIV-specific synthetic oligonucleotide and method of using the same

FEATURES FH Key location/Qualifiers
FT source 1..21
/organism='Human immunodeficiency virus'.
Location/Qualifiers
1..21
/organism='Human immunodeficiency virus'
/mol_type='genomic DNA'
/db_xref='taxon:12721'

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCCATCTCTCTCTCT 21
1 CGACCCATCTCTCTCTCT 21

Db 1 CGACCCATCTCTCTCTCT 21

RESULT 3
BD077066 21 bp DNA linear PAT 27-AUG-2002
LOCUS Novel HIV-specific synthetic oligonucleotide and method of using the same.
DEFINITION BD077066
ACCESSION BD077066
VERSION BD077066.1 GI:22622669
KEYWORDS JP 2001514884-A/4;
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.
1 (bases 1 to 21)

REFERENCE Agrawal, S.
AUTHORS Novel HIV-specific synthetic oligonucleotide and method of using the same
TITLE Patent: JP 2001514884-A 4 18-SEP-2001;
JOURNAL HYBRIDON INC

COMMENT OS Human immunodeficiency virus
PN JP 2001514884-A/4
PD 18-SEP-2001
PR 05-AUG-1998 JP 2000509820
PR 19-AUG-1997 US 08/914827
PI SUDHIR AGRAWAL
PC C12N15/09,A61K31/7125,A61P31/18,C12N15/00
CC Novel HIV-specific synthetic oligonucleotide and method of using the same

FEATURES FH Key location/Qualifiers
FT source 1..21
/organism='Human immunodeficiency virus'.
Location/Qualifiers
1..21
/organism='Human immunodeficiency virus'
/mol_type='genomic DNA'
/db_xref='taxon:12721'

ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCCATCTCTCTCTCT 21
1 CGACCCATCTCTCTCTCT 21

Db 1 CGACCCATCTCTCTCTCT 21

RESULT 4
149132 22 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 6 from patent US 5627277.
DEFINITION 149132
ACCESSION 149132
VERSION 149132.1 GI:2467595
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 22)
AUTHORS Cohen, A.S., Bourque, A. and Vilenchik, M.
TITLE Method for analyzing oligonucleotide analogs
JOURNAL Patent: US 5627277-A 6 06-MAY-1997;
FEATURES Location/Qualifiers
source 1..22
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ORIGIN

Query Match 100.0%; Score 21; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 CGACCCATCTCTCTCTCT 22

RESULT 5
BD077067 22 bp DNA linear PAT 27-AUG-2002
LOCUS Novel HIV-specific synthetic oligonucleotide and method of using the same.
DEFINITION BD077067
ACCESSION BD077067
VERSION BD077067.1 GI:22622670
KEYWORDS JP 2001514884-A/5;
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group.
1 (bases 1 to 22)

REFERENCE Agrawal, S.
AUTHORS Novel HIV-specific synthetic oligonucleotide and method of using the same
TITLE Patent: JP 2001514884-A 5 18-SEP-2001;
JOURNAL HYBRIDON INC

COMMENT OS Human immunodeficiency virus
PN JP 2001514884-A/5
PD 18-SEP-2001
PR 05-AUG-1998 JP 2000509820
PR 19-AUG-1997 US 08/914827
PI SUDHIR AGRAWAL
PC C12N15/09,A61K31/7125,A61P31/18,C12N15/00
CC Novel HIV-specific synthetic oligonucleotide and method of using the same

FEATURES FH Key location/Qualifiers
FT source 1..22
/organism='Human immunodeficiency virus'.
Location/Qualifiers
1..22
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGACCCATCTCTCTCTCT 21
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Db 2 CGACCCATCTCTCTCTCT 22
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RESULT 6
LOCUS 149134 20 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 8 from patent US 5627277.
ACCESSION 149134
VERSION 149134.1 GI:2467597
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cohen, A.S., Bourque, A. and Vilenchik, M.
TITLE Method for analyzing oligonucleotide analogs
JOURNAL Patent: US 5627277-A 8 06-MAY-1997;
FEATURES Location/Qualifiers
source 1..20
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Best Local Similarity 100.0%; Pred. No. 25;
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Db 1 GCACCCATCTCTCTCTCT 20
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RESULT 7
LOCUS AX146648 21 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 2 from Patent WO0134093.
ACCESSION AX146648
VERSION AX146648.1 GI:14285041
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Agrawal, S.
TITLE Potential of prodrg efficacy
JOURNAL Patent: WO 0134093-A 2 17-MAY-2001;
HYBRIDON, INC. (US)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="oligonucleotide sequence"

ORIGIN
Query Match 95.2%; Score 20; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGACCCATCTCTCTCTTC 20
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Db 2 CGACCCATCTCTCTCTTC 21
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RESULT 8
LOCUS AX203700 21 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 35 from Patent WO0152304.

ACCESSION AX203700
VERSION AX203700.1 GI:15393146
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Gill, P.S. and Masood, R.
TITLE Methods and compositions for antisense vegf oligonucleotides
JOURNAL Patent: WO 0152904-A 35 26-JUL-2001;
Gill, Parkash, S. (US)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
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nucleotides 1-4 and 18-21 and 2' O methylribonucleosides"

ORIGIN
Query Match 95.2%; Score 20; DB 6; Length 21;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 CGACCCATCTCTCTCTTC 21
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RESULT 9
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DEFINITION Novel HIV-specific synthetic oligonucleotide and method of using
the same.
ACCESSION BD077063
VERSION BD077063.1 GI:22622666
KEYWORDS UP 2001514884-A/1.
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
REFERENCE 1
AUTHORS Agrawal, S.
TITLE Novel HIV-specific synthetic oligonucleotide and method of using
the same
JOURNAL Patent: JP 2001514884-A 1 18-SEP-2001;
HYBRIDON INC
COMMENT OS Human immunodeficiency virus
PN JP 2001514884-A/1
PD 18-SEP-2001
PF 05-AUG-1998 JP 2000509820
PR 19-AUG-1997 US 08/914827
PI SUDHIR AGRAWAL
PC C12N15/09, A61K31/7125, A61P31/18, C12N15/00
CC Novel HIV-specific synthetic oligonucleotide and method of CC
using the same
FH Key Location/Qualifiers
FT source 1..21
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/mol_type="genomic DNA"
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Db 2 CGACCCATCTCTCTCTTC 21
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RESULT 10
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ACCESSION BD077064
VERSION BD077064.1 GI:22622667
KEYWORDS JP 2001514884-A/2.
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
VIRUSES; Retroviral viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 21)
REFERENCE
AUTHORS Agrawal,S.
TITLE Novel HIV-specific synthetic oligonucleotide and method of using
the same.
JOURNAL Patent: JP 2001514884-A 2 18-SEP-2001;
HYBRIDON INC
OS Human immunodeficiency virus
PN JP 2001514884-A/2
PD 18-SEP-2001
PR 05-AUG-1998 JP 2000509820
PI 19-AUG-1997 US 08/914827
PC C12N15/09,A61K31/7125,A61P31/18,C12N15/00
CC Novel HIV-specific synthetic oligonucleotide and method of
using the same
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Db 2 CGACCCATCTCTCTCTTC 21

RESULT 11
BD077068
LOCUS
DEFINITION Novel HIV-specific synthetic oligonucleotide and method of using
the same.
ACCESSION BD077068
VERSION BD077068.1 GI:22622671
KEYWORDS JP 2001514884-A/6.
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
VIRUSES; Retroviral viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
1 (bases 1 to 21)
REFERENCE
AUTHORS Agrawal,S.
TITLE Novel HIV-specific synthetic oligonucleotide and method of using
the same.
JOURNAL Patent: JP 2001514884-A 6 18-SEP-2001;
HYBRIDON INC
OS Human immunodeficiency virus
PN JP 2001514884-A/6
PD 18-SEP-2001
PR 05-AUG-1998 JP 2000509820
PI 19-AUG-1997 US 08/914827
PC C12N15/09,A61K31/7125,A61P31/18,C12N15/00

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CC Novel HIV-specific synthetic oligonucleotide and method of
using the same
FH Key Location/Qualifiers
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ORIGIN
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Db 2 CGACCCATCTCTCTCTTC 21

RESULT 12
AR170398
LOCUS AR170398 22 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 24 from patent US 6291438.
ACCESSION AR170398
VERSION AR170398.1 GI:17908357
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Wang,J.H.
TITLE Antiviral anticancer poly-substituted phenyl derivatized
oligonucleotides and methods for their use
JOURNAL Patent: US 6291438-A 24 18-SEP-2001;
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Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 GCACCCATCTCTCTCTCT 21

RESULT 13
AR206325
LOCUS AR206325 21 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from patent US 6372427.
ACCESSION AR206325
VERSION AR206325.1 GI:21504894
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Kandimala,B.R. and Agrawal,S.
TITLE Cooperative oligonucleotides
JOURNAL Patent: US 6372427-A 5 16-APR-2002;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 82;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
AR374987
LOCUS AR374987 21 bp mRNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6605708.
ACCESSION AR374987
VERSION AR374987.1 GI:40078169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 21)
Habus, I. and Agrawal, S.
TITLE Building blocks with carbamate internucleoside linkages and
oligonucleotides derived therefrom
JOURNAL Patent: US 6605708-A 1 12-AUG-2003;
FEATURES
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DEFINITION Sequence 8 from patent US 6207455.
ACCESSION AR140320
VERSION AR140320.1 GI:14482816
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 22)
AUTHORS Chang, L.-J.
TITLE Lentiviral vectors
JOURNAL Patent: US 6207455-A 8 27-MAR-2001;
FEATURES
location/Qualifiers
source 1..22
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/mol_type="unassigned DNA"

ORIGIN

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QY 1 CGCACCACATCTCTCTCCTTC 20
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Db 20 CGCACCACATCTCTCTCCTTC 1

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Job time : 773.628 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2005, 21:36:56; Search time 70.6047 Seconds
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Perfect score: 22
Sequence: 1 tcgacccatctctctctctct 22

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 487750

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	22	100.0	22	5	PCT-US95-00163-6
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4	21	95.5	21	5	PCT-US95-00163-7
5	20	90.9	20	1	US-08-178-660-8
6	20	90.9	20	5	PCT-US95-00163-8
7	20	90.9	21	3	US-08-420-672-5
8	20	90.9	21	4	US-08-098-945A-1
9	20	90.9	22	3	US-09-167-375-24
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12	19.4	88.2	22	4	US-09-318-138-8
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14	19	86.4	20	4	US-08-664-786-1
15	19	86.4	20	4	US-08-664-786-2
16	19	86.4	20	4	US-08-664-786-18
17	19	86.4	20	5	PCT-US95-06720-1
18	19	86.4	20	5	PCT-US95-06720-2
19	19	86.4	22	4	US-09-587-934B-19
20	19	86.4	22	4	US-09-321-249-19
21	19	86.4	22	4	US-08-420-672-23
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24	17	77.3	17	4	US-09-605-558B-75
25	17	77.3	17	5	PCT-US95-06379-32
26	17	77.3	20	2	US-08-790-963-50
27	17	77.3	20	2	US-08-790-963-50

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	29	17	77.3	20	3	US-09-371-774-50	Sequence 50, Appl
	30	17	77.3	20	5	PCT-US95-06161-2	Sequence 2, Appl
	31	17	77.3	20	5	PCT-US95-06161-3	Sequence 3, Appl
	32	16.8	76.4	21	3	US-08-420-672-24	Sequence 24, Appl
	33	16	72.7	19	1	US-08-473-096-22	Sequence 22, Appl
	34	15.4	70.0	20	3	US-09-166-186-51	Sequence 51, Appl
	35	15.4	70.0	20	3	US-09-313-992-51	Sequence 51, Appl
	36	15	68.2	19	1	US-08-241-062-2	Sequence 2, Appl
	37	14.4	65.5	19	1	US-08-473-096-20	Sequence 20, Appl
	38	14.4	65.5	22	4	US-09-871-579-1	Sequence 1, Appl
	39	14.2	64.5	19	3	US-08-420-672-13	Sequence 13, Appl
	40	14.2	64.5	21	1	US-07-988-194A-24	Sequence 24, Appl
	41	14.2	64.5	21	1	US-08-258-152-26	Sequence 26, Appl
	42	14.2	64.5	21	2	US-08-076-299A-26	Sequence 26, Appl
	43	14.2	64.5	21	2	US-08-438-582-26	Sequence 26, Appl
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ALIGNMENTS

RESULT 1
US-08-178-660-6
; Sequence 6, Application US/08178660
; Patent No. 5627277
; GENERAL INFORMATION:
; APPLICANT: Cohen, Aharon S.
; APPLICANT: Bourque, Andre
; APPLICANT: Vilenchik, Maria
; TITLE OF INVENTION: Method for Analyzing
; TITLE OF INVENTION: Oligonucleotide Analogs
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Lappin & Kusner
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,660
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Keiner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/330-1300
; TELEFAX: 617/330-1311
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; US-08-178-660-6

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Db 1 TCGACCCATCTCTCTCTTCT 22

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PCT-US95-00163-6

/ Sequence 6, Application PC/TUS9500163

/ GENERAL INFORMATION:

/ APPLICANT: Cohen, Aharon S.

/ APPLICANT: Bourque, Andre

/ APPLICANT: Vilenchik, Maria

/ TITLE OF INVENTION: Method for Analyzing

/ TITLE OF INVENTION: Oligonucleotide Analogs

/ NUMBER OF SEQUENCES: 8

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Lappin & Kusmer

/ STREET: 200 State Street

/ CITY: Boston

/ STATE: Massachusetts

/ COUNTRY: U.S.A.

/ ZIP: 02109

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: PCT/US95/00163

/ FILING DATE:

/ CLASSIFICATION:

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Kermer, Ann-Louise

/ REGISTRATION NUMBER: 33,523

/ REFERENCE/DOCKET NUMBER: HYZ-012PCT

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 617/330-1300

/ TELEFAX: 617/330-1311

/ INFORMATION FOR SEQ ID NO: 6:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 22 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: CDNA

/ HYPOTHETICAL: NO

/ PCT-US95-00163-6

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/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/178,660

/ FILING DATE:

/ CLASSIFICATION: 536

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Kermer, Ann-Louise

/ REGISTRATION NUMBER: 33,523

/ REFERENCE/DOCKET NUMBER: HYZ-012

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 617/330-1300

/ TELEFAX: 617/330-1311

/ INFORMATION FOR SEQ ID NO: 7:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 21 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

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Query Match 95.5%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1;
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Db 2 CGACCCATCTCTCTCTTCT 22
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RESULT 4

PCT-US95-00163-7

/ Sequence 7, Application PC/TUS9500163

/ GENERAL INFORMATION:

/ APPLICANT: Cohen, Aharon S.

/ APPLICANT: Bourque, Andre

/ APPLICANT: Vilenchik, Maria

/ TITLE OF INVENTION: Method for Analyzing

/ TITLE OF INVENTION: Oligonucleotide Analogs

/ NUMBER OF SEQUENCES: 8

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Lappin & Kusmer

/ STREET: 200 State Street

/ CITY: Boston

/ STATE: Massachusetts

/ COUNTRY: U.S.A.

/ ZIP: 02109

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent In Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: PCT/US95/00163

/ FILING DATE:

/ CLASSIFICATION:

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Kermer, Ann-Louise

/ REGISTRATION NUMBER: 33,523

/ REFERENCE/DOCKET NUMBER: HYZ-012PCT

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 617/330-1300

/ TELEFAX: 617/330-1311

/ INFORMATION FOR SEQ ID NO: 7:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 21 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

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TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
PCT-US95-00163-7

Query Match 95.5%; Score 21; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCACCCATCTCTCTCTCT 21

RESULT 5
US-08-178-660-8

Sequence 8, Application US/08178660
Patent No. 5627277

GENERAL INFORMATION:

APPLICANT: Cohen, Aaron S.

APPLICANT: Bourque, Andre

APPLICANT: Valenchik, Maria

TITLE OF INVENTION: Method for Analyzing

TITLE OF INVENTION: Oligonucleotide Analogs

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lappin & Kusner

STREET: 200 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/178,660

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HYZ-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/330-1300

TELEFAX: 617/330-1311

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

US-08-178-660-8

Query Match 90.9%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCACCCATCTCTCTCTCT 22

DB 1 GCACCCATCTCTCTCTCT 20

RESULT 6
PCT-US95-00163-8
Sequence 8, Application PC/TUS9500163
GENERAL INFORMATION:
APPLICANT: Cohen, Aaron S.
APPLICANT: Bourque, Andre

APPLICANT: Valenchik, Maria
TITLE OF INVENTION: Method for Analyzing
TITLE OF INVENTION: Oligonucleotide Analogs
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lappin & Kusner

STREET: 200 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/00163

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HYZ-012PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/330-1300

TELEFAX: 617/330-1311

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

PCT-US95-00163-8

Query Match 90.9%; Score 20; DB 5; Length 20;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCACCCATCTCTCTCTCT 22

DB 1 GCACCCATCTCTCTCTCT 20

RESULT 7
US-08-420-672-5

Sequence 5, Application US/08420672

Patent No. 6372427

GENERAL INFORMATION:

APPLICANT: Kandimala, Ekambar R.

APPLICANT: Agrawal, Sudhir

TITLE OF INVENTION: COOPERATIVE OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lappin & Kusner

STREET: 200 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/420,672

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HY2-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-420-672-5

Query Match 90.9%; Score 20; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTT 20
Db 2 TCGACCCATCTCTCTCTT 21

RESULT 8
US-08-098-945A-1

Sequence 1, Application US/08098945A

Patent No. 6605708

GENERAL INFORMATION:

APPLICANT: Habus, Ivan

AGRAWAL, Sudhir

TITLE OF INVENTION: Building Blocks with Carbamate

Intermolecular Linkages and No. 6605708el Oligonucleotides

Derived Therefrom

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr LLP

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: United States

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/098,945A

FILING DATE: 28-Jul-1993

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HY2-027 (47508-498)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-6000

TELEFAX: (617) 526-5000

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 90.9%; Score 20; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTT 20
Db 2 TCGACCCATCTCTCTCTT 21

RESULT 9
US-09-167-375-24

Sequence 24, Application US/09167375B

Patent No. 6291438

GENERAL INFORMATION:

APPLICANT: Jui H. Wang

TITLE OF INVENTION: Antiviral anticancer poly-substituted phenyl derivatized oligorib

FILE REFERENCE: WNGJ 2002 (CIP-1)

CURRENT APPLICATION NUMBER: US/09/167,375B

CURRENT FILING DATE: 1998-10-06

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 24

LENGTH: 22

TYPE: RNA

ORGANISM: Human Immunodeficiency Virus type 1

FEATURE:

LOCATION: Portion of the gag gene

OTHER INFORMATION: Complementary to a portion of the gag gene

US-09-167-375-24

Query Match 90.9%; Score 20; DB 3; Length 22;
Best Local Similarity 65.0%; Pred. No. 5.8;
Matches 13; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCACCCATCTCTCTCTT 22
Db 2 GCACCCATCTCTCTCTT 21

RESULT 10
US-08-935-312-8/C

Sequence 8, Application US/08935312

Patent No. 6207455

GENERAL INFORMATION:

APPLICANT: CHANG, Lung-Ji

TITLE OF INVENTION: LENTIVIRAL VECTORS

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.

STREET: 624 Ninth Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/935,312

FILING DATE: 22-SEP-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: CHANG-112

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-935-312-8

Query Match 88.2%; Score 19.4; DB 3; Length 22;
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGACCCACTCTCTCTCTTC 21
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DB 21 TCGACCCCACTCTCTCTTC 1

RESULT 11

US-08-420-672-6
Sequence 6, Application US/08420672
Patent No. 6372427
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: COOPERATIVE OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/420,672
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-027
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-420-672-6

Query Match 88.2%; Score 19.4; DB 3; Length 22;
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGACCCACTCTCTCTCTTC 21
|||||
DB 2 TCGACCCGCTCTCTCTCTTC 22

RESULT 12

US-09-318-138-8/c
Sequence 8, Application US/09318138
Patent No. 6531123
GENERAL INFORMATION:
APPLICANT: CHANG, Lung-Ji
TITLE OF INVENTION: LENTIVIRAL VECTORS

NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/318,138
FILING DATE: 25-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/086,635
FILING DATE: 26-MAY-1998
APPLICATION NUMBER: US 08/935,312
FILING DATE: 22-SEP-1997

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: CHANG-109A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-318-138-8

Query Match 88.2%; Score 19.4; DB 4; Length 22;
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGACCCACTCTCTCTCTTC 21
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DB 21 TCGACCCCACTCTCTCTTC 1

RESULT 13

US-08-319-823A-10
Sequence 10, Application US/08319823A
Patent No. 5684147
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Therapeutic Anti-HIV Antiviral
TITLE OF INVENTION: Oligonucleotides and Pharmaceutical Formulations Thereof
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff, Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft Word for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,823A
FILING DATE: 10/7/94
CLASSIFICATION: 514

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/ ATTORNEY/AGENT INFORMATION:
/ NAME: Greenfield, Michael S.
/ REGISTRATION NUMBER: 37,142
/ REFERENCE/DOCKET NUMBER: 92,623-B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-9808
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: CDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: YES
/ FEATURE:
/ NAME/KEY: GEM 90
/ LOCATION: complementary to bp 327-346 of HIV-1 DNA
/
US-08-319-823A-10

Query Match
Best Local Similarity 86.4%; Score 19; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGACCCATCTCTCTCT 19
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Db 2 TCGACCCATCTCTCTCT 20

RESULT 14
US-08-664-786-1
/ Sequence 1, Application US/08664786
/ Patent No. 6489464
/ GENERAL INFORMATION:
/ APPLICANT: Meschwitz, Susan M.
/ APPLICANT: Agrawal, Sudhir
/ TITLE OF INVENTION: Branched Oligonucleotides as Pathogen
/ TITLE OF INVENTION: Inhibitory Agents
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Michael S. Greenfield
/ STREET: 10 S. Wacker Drive Suite 3000
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: U.S.A.
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Wordperfect for DOS 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/664,786
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION NUMBER: US/08/252,494
/ APPLICATION DATA:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Greenfield, Michael S.
/ REGISTRATION NUMBER: 37,142
/ REFERENCE/DOCKET NUMBER: 93,743
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312)715-1000
/ TELEFAX: (312)715-1234
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ HYPOTHETICAL: NO
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/ ANTI-SENSE: YES
/
US-08-664-786-1

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Best Local Similarity 86.4%; Score 19; DB 4; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGACCCATCTCTCTCT 19
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Db 2 TCGACCCATCTCTCTCT 20

RESULT 15
US-08-664-786-2
/ Sequence 2, Application US/08664786
/ Patent No. 6489464
/ GENERAL INFORMATION:
/ APPLICANT: Meschwitz, Susan M.
/ APPLICANT: Agrawal, Sudhir
/ TITLE OF INVENTION: Branched Oligonucleotides as Pathogen
/ TITLE OF INVENTION: Inhibitory Agents
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Michael S. Greenfield
/ STREET: 10 S. Wacker Drive Suite 3000
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: U.S.A.
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Wordperfect for DOS 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/664,786
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/252,494
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Greenfield, Michael S.
/ REGISTRATION NUMBER: 37,142
/ REFERENCE/DOCKET NUMBER: 93,743
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312)715-1000
/ TELEFAX: (312)715-1234
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ HYPOTHETICAL: NO
/ ANTI-SENSE: YES
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1..20
/ OTHER INFORMATION: /note="All phosphothioate
/ OTHER INFORMATION: internucleotide linkages"
/
US-08-664-786-2

Query Match
Best Local Similarity 86.4%; Score 19; DB 4; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 2 TCGACCCATCTCTCTCT 20
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-896-692b-5

Perfect score: 22
Sequence: 1 tcgcaccatctctctctctct 22

Scoring table: IDENTITY NUC
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Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	95.5	21	9	US-09-805-761-35
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6	21	95.5	21	10	US-09-896-692b-4
7	21	95.5	21	10	US-09-896-692b-6

8	21	95.5	21	15	US-10-262-318-11	Sequence 11, Appl
9	20	90.9	21	14	US-10-054-429a-5	Sequence 5, Appl
10	19	88.2	22	14	US-10-054-429a-6	Sequence 6, Appl
11	19	86.4	19	16	US-10-225-023-420	Sequence 420, App
12	19	86.4	19	16	US-10-225-023-429	Sequence 429, App
13	19	86.4	19	16	US-10-225-023-440	Sequence 440, App
14	19	86.4	19	16	US-10-225-023-466	Sequence 466, App
15	19	86.4	19	16	US-10-225-023-1158	Sequence 1158, App
16	19	86.4	19	16	US-10-225-023-1167	Sequence 1167, App
17	19	86.4	19	16	US-10-225-023-1178	Sequence 1178, App
18	19	86.4	19	16	US-10-225-023-1204	Sequence 1204, App
19	19	86.4	19	22	US-10-923-473-420	Sequence 429, App
20	19	86.4	19	22	US-10-923-473-429	Sequence 429, App
21	19	86.4	19	22	US-10-923-473-440	Sequence 440, App
22	19	86.4	19	22	US-10-923-473-466	Sequence 466, App
23	19	86.4	19	22	US-10-923-473-1158	Sequence 1158, App
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25	19	86.4	19	22	US-10-923-473-1178	Sequence 1178, App
26	19	86.4	19	22	US-10-923-473-1204	Sequence 1204, App
27	19	86.4	20	16	US-10-292-148-31	Sequence 31, Appl
28	19	86.4	20	16	US-10-292-149-31	Sequence 31, Appl
29	19	86.4	22	18	US-10-640-898-19	Sequence 19, Appl
30	18	83.6	21	14	US-10-054-429a-23	Sequence 23, Appl
31	18	81.8	18	20	US-10-483-654-18	Sequence 18, Appl
32	18	81.8	19	16	US-10-225-023-409	Sequence 409, App
33	18	81.8	19	16	US-10-225-023-463	Sequence 463, App
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38	18	81.8	19	22	US-10-923-473-1147	Sequence 1147, App
39	18	81.8	19	22	US-10-923-473-1201	Sequence 1201, App
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43	17	77.3	17	15	US-10-157-580a-61	Sequence 61, Appl
44	17	77.3	17	15	US-10-157-580a-69	Sequence 69, Appl
45	17	77.3	17	15	US-10-157-580a-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-09-896-692b-5
; Sequence 5, Application US/09896692b
; Publication No. US20030100521a1
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: No. US20030100521a1 HIV-Specific Synthetic Oligonucleotides and
TITLE OF INVENTION: Methods of Their Use
FILE REFERENCE: 47508.556 (HYZ-069)
CURRENT APPLICATION NUMBER: US/09/896, 692b
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 08/914, 827
PRIOR FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic modified antisense oligonucleotide
US-09-896-692b-5

Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3; Mismatches 0; Gaps 0;
Matches 22; Conservative 0; Indels 0;
DB 1 TCgcaccatctctctctct 22
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RESULT 2
US-09-805-761-35
; Sequence 35, Application US/09805761
; Patent No. US2002016517A1
; GENERAL INFORMATION:
; APPLICANT: GILL, Parkesh
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; FILE REFERENCE: 21327-701CON2
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Scrambled mixed backbone oligonucleotides,
; OTHER INFORMATION: nucleotides 1-4 and 18-21 and 2'0
US-09-805-761-35

Query Match          95.5%; Score 21; DB 9; Length 21;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGACCCATCTCTCTCCTTC 21
Db      1 UCGACCCATCTCTCTCCUUC 21

RESULT 3
US-09-896-692B-1
; Sequence 1, Application US/09896692B
; Publication No. US20030100521A1
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: No. US20030100521A1el HIV-Specific Synthetic Oligonucleotides and
; FILE REFERENCE: 47508.556 (HYZ-069)
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/896,692B
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 08/914,827
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: DNA/RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic modified antisense oligonucleotide
US-09-896-692B-1

Query Match          95.5%; Score 21; DB 10; Length 21;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGACCCATCTCTCTCCTTC 21
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Db      1 UCGACCCATCTCTCTCCUUC 21

RESULT 4
US-09-896-692B-2
; Sequence 2, Application US/09896692B
; Publication No. US20030100521A1
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: No. US20030100521A1el HIV-Specific Synthetic Oligonucleotides and
; FILE REFERENCE: 47508.556 (HYZ-069)
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/896,692B
; PRIOR FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic modified antisense oligonucleotide
US-09-896-692B-2

Query Match          95.5%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGACCCATCTCTCTCCTTC 21
Db      1 TCGACCCATCTCTCTCCTTC 21

RESULT 5
US-09-896-692B-3
; Sequence 3, Application US/09896692B
; Publication No. US20030100521A1
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: No. US20030100521A1el HIV-Specific Synthetic Oligonucleotides and
; FILE REFERENCE: 47508.556 (HYZ-069)
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/896,692B
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 08/914,827
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA/RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic modified antisense oligonucleotide
US-09-896-692B-3

Query Match          95.5%; Score 21; DB 10; Length 21;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGACCCATCTCTCTCCTTC 22
Db      1 CGACCCATCTCTCTCCUUC 21

RESULT 6
US-09-896-692B-4
; Sequence 4, Application US/09896692B
; Publication No. US20030100521A1
; GENERAL INFORMATION:
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; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: No. US20030100521A1el HIV-specific Synthetic Oligonucleotides and
; FILE REFERENCE: 47508.556 (HYZ-069)
; CURRENT APPLICATION NUMBER: US/09/896,692B
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 08/914,827
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic modified antisense oligonucleotide
US-09-896-692B-4

Query Match          95.5%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGCACCCATCTCTCTCTCT 22
DB 1 CGCACCCATCTCTCTCTCT 21

RESULT 7
US-09-896-692B-6
; Sequence 6, Application US/09896692B
; Publication No. US20030100521A1
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: No. US20030100521A1el HIV-specific Synthetic Oligonucleotides and
; FILE REFERENCE: 47508.556 (HYZ-069)
; CURRENT APPLICATION NUMBER: US/09/896,692B
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 08/914,827
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 21
; TYPE: DNA/RNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic modified oligonucleotide
US-09-896-692B-6

Query Match          95.5%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTC 21
DB 1 TCGACCCATCTCTCTCTTC 21

RESULT 8
US-10-262-318-11
; Sequence 11, Application US/10262318
; Publication No. US20030144198A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Douglas A.
; TITLE OF INVENTION: COPIES OF TRANSPORT PROTEINS WITH CONJUGATED COBALAMIN
; FILE REFERENCE: COP1012
; CURRENT APPLICATION NUMBER: US/10/262,318
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: artificial sequence
; OTHER INFORMATION: oligonucleotide-- GEM-92 (Hybridon)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(4)
; OTHER INFORMATION: 2' Ome sugar modifications
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (18)..(21)
; OTHER INFORMATION: 2' Ome sugar modifications
US-10-262-318-11

Query Match          95.5%; Score 21; DB 15; Length 21;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTC 21
DB 1 UCGACCCATCTCTCTCUC 21

RESULT 9
US-10-054-429A-5
; Sequence 5, Application US/10054429A
; Publication No. US2003009959A1
; GENERAL INFORMATION:
; APPLICANT: Kandimala, Ekambar R.
; TITLE OF INVENTION: Cooperative Oligonucleotides
; FILE REFERENCE: 47508-580 (HYZ-027CIP)
; CURRENT APPLICATION NUMBER: US/10/054,429A
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 08/420,672
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: cooperative oligonucleotide
US-10-054-429A-5

Query Match          90.9%; Score 20; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTT 20
DB 2 TCGACCCATCTCTCTCTT 21

RESULT 10
US-10-054-429A-6
; Sequence 6, Application US/10054429A
; Publication No. US2003009959A1
; GENERAL INFORMATION:
; APPLICANT: Kandimala, Ekambar R.
; TITLE OF INVENTION: Cooperative Oligonucleotides
; FILE REFERENCE: 47508-580 (HYZ-027CIP)
; CURRENT APPLICATION NUMBER: US/10/054,429A
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 08/420,672
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
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/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: cooperative oligonucleotide
US-10-054-429A-6

Query Match 88.2%; Score 19.4; DB 14; Length 22;
Best Local Similarity 95.2%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGACCCATCTCTCTCTTC 21
 |||||
Db 2 TCGACCCGCTCTCTCTCTTC 22

RESULT 11
US-10-225-023-420/c
/ Sequence 420, Application US/10225023
/ Publication No. US20030175950A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: McSwiggen, James
/ TITLE OF INVENTION: RNA Interference Mediated Inhibition of HIV Gene Expression Using
/ FILE REFERENCE: 400/054 (MBH01-665-B)
/ CURRENT APPLICATION NUMBER: US/10/225,023
/ PRIOR FILING DATE: 2003-01-06
/ PRIOR APPLICATION NUMBER: US 60/398,036
/ PRIOR FILING DATE: 2002-07-23
/ PRIOR APPLICATION NUMBER: US 60/294,140
/ PRIOR FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: US 10/157,580
/ NUMBER OF SEQ ID NOS: 1494
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 420
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-225-023-420

Query Match 86.4%; Score 19; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCACCCATCTCTCTCTTC 21
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Db 19 GCACCCATCTCTCTCTTC 1

RESULT 12
US-10-225-023-429/c
/ Sequence 429, Application US/10225023
/ Publication No. US20030175950A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: McSwiggen, James
/ TITLE OF INVENTION: RNA Interference Mediated Inhibition of HIV Gene Expression Using
/ FILE REFERENCE: 400/054 (MBH01-665-B)
/ CURRENT APPLICATION NUMBER: US/10/225,023
/ PRIOR FILING DATE: 2003-01-06
/ PRIOR APPLICATION NUMBER: US 60/398,036
/ PRIOR FILING DATE: 2002-07-23
/ PRIOR APPLICATION NUMBER: US 60/294,140
/ PRIOR FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: US 10/157,580
/ NUMBER OF SEQ ID NOS: 1494
/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 429
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-225-023-429

Query Match 86.4%; Score 19; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGACCCATCTCTCTCTT 20
 |||||
Db 19 CGACCCATCTCTCTCTT 1

RESULT 13
US-10-225-023-440/c
/ Sequence 440, Application US/10225023
/ Publication No. US20030175950A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: McSwiggen, James
/ TITLE OF INVENTION: RNA Interference Mediated Inhibition of HIV Gene Expression Using
/ FILE REFERENCE: 400/054 (MBH01-665-B)
/ CURRENT APPLICATION NUMBER: US/10/225,023
/ PRIOR FILING DATE: 2003-01-06
/ PRIOR APPLICATION NUMBER: US 60/398,036
/ PRIOR FILING DATE: 2002-07-23
/ PRIOR APPLICATION NUMBER: US 60/294,140
/ PRIOR FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: US 10/157,580
/ NUMBER OF SEQ ID NOS: 1494
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 440
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-225-023-440

Query Match 86.4%; Score 19; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGACCCATCTCTCTCT 19
 |||||
Db 19 TCGACCCATCTCTCTCT 1

RESULT 14
US-10-225-023-466/c
/ Sequence 466, Application US/10225023
/ Publication No. US20030175950A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: McSwiggen, James
/ TITLE OF INVENTION: RNA Interference Mediated Inhibition of HIV Gene Expression Using
/ FILE REFERENCE: 400/054 (MBH01-665-B)
/ CURRENT APPLICATION NUMBER: US/10/225,023
/ PRIOR FILING DATE: 2003-01-06
/ PRIOR APPLICATION NUMBER: US 60/398,036
/ PRIOR FILING DATE: 2002-07-23
/ PRIOR APPLICATION NUMBER: US 60/294,140
/ PRIOR FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: US 10/157,580
/ NUMBER OF SEQ ID NOS: 1494

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/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 466
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-225-023-466

Query Match                      86.4%; Score 19; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CACCCATCTCTCCTTCT 22
         |||||
Db       19 CACCCATCTCTCCTTCT 1

RESULT 15
US-10-225-023-1158
/ Sequence 1158, Application US/10225023
/ Publication No. US20030175950A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: MCSwigen, James
/ TITLE OF INVENTION: RNA Interference Mediated Inhibition of HIV Gene Expression Using
/ FILE REFERENCE: 400/054 (MEH01-665-B)
/ CURRENT FILING DATE: 2003-01-06
/ PRIOR APPLICATION NUMBER: US/10/225,023
/ PRIOR FILING DATE: 2002-07-23
/ PRIOR APPLICATION NUMBER: US 60/398,036
/ PRIOR FILING DATE: 2002-05-29
/ PRIOR APPLICATION NUMBER: US 10/157,580
/ PRIOR FILING DATE: 2002-05-29
/ NUMBER OF SEQ ID NOS: 1494
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1158
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-225-023-1158

Query Match                      86.4%; Score 19; DB 16; Length 19;
Best Local Similarity 68.4%; Pred. No. 89;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCACCATCTCTCTCTTC 21
         |||||
Db       1 GCACCAUCUCUCUCCUCC 19
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OM nucleic - nucleic search, using sw model

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Title: US-09-896-692B-5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	10 US-08-478-464-6	Sequence 6, Appl1
2	22	100.0	22	15 US-08-914-827-5	Sequence 5, Appl1
3	22	100.0	22	36 US-09-837-806-5	Sequence 5, Appl1
4	22	100.0	22	36 US-09-837-806A-5	Sequence 5, Appl1
5	22	100.0	22	38 US-09-896-692B-5	Sequence 5, Appl1
6	21	95.5	21	10 US-08-478-464-7	Sequence 7, Appl1
7	21	95.5	21	15 US-08-914-827-1	Sequence 1, Appl1
8	21	95.5	21	15 US-08-914-827-2	Sequence 2, Appl1
9	21	95.5	21	15 US-08-914-827-3	Sequence 3, Appl1
10	21	95.5	21	15 US-08-914-827-4	Sequence 4, Appl1
11	21	95.5	21	32 US-08-708-786-2	Sequence 2, Appl1
12	21	95.5	21	35 US-09-805-761-35	Sequence 35, Appl1
13	21	95.5	21	36 US-09-837-806-1	Sequence 1, Appl1
14	21	95.5	21	36 US-09-837-806-2	Sequence 2, Appl1
15	21	95.5	21	36 US-09-837-806-3	Sequence 3, Appl1
16	21	95.5	21	36 US-09-837-806-4	Sequence 4, Appl1
17	21	95.5	21	36 US-09-837-806-6	Sequence 6, Appl1
18	21	95.5	21	36 US-09-837-806A-1	Sequence 1, Appl1
19	21	95.5	21	36 US-09-837-806A-2	Sequence 2, Appl1
20	21	95.5	21	36 US-09-837-806A-3	Sequence 3, Appl1
21	21	95.5	21	36 US-09-837-806A-4	Sequence 4, Appl1
22	21	95.5	21	36 US-09-837-806A-6	Sequence 6, Appl1
23	21	95.5	21	38 US-09-896-692B-1	Sequence 1, Appl1
24	21	95.5	21	38 US-09-896-692B-2	Sequence 2, Appl1
25	21	95.5	21	38 US-09-896-692B-3	Sequence 3, Appl1
26	21	95.5	21	38 US-09-896-692B-4	Sequence 4, Appl1
27	21	95.5	21	38 US-09-896-692B-6	Sequence 6, Appl1
28	21	95.5	21	48 US-10-140-278-29	Sequence 29, Appl1
29	21	95.5	21	50 US-10-246-300D-29	Sequence 29, Appl1
30	21	95.5	21	51 US-10-262-318-11	Sequence 11, Appl1
31	21	95.5	21	51 US-10-262-318-11	Sequence 11, Appl1
32	20	90.9	20	10 US-08-478-464-8	Sequence 8, Appl1
33	20	90.9	21	1 PCT-US94-08655-1	Sequence 1, Appl1
34	20	90.9	21	1 PCT-US03-01814-5	Sequence 5, Appl1
35	20	90.9	21	12 US-08-627-967-5	Sequence 5, Appl1
36	20	90.9	21	13 US-08-751-384-5	Sequence 5, Appl1
37	20	90.9	21	47 US-10-054-429A-5	Sequence 5, Appl1
38	19.4	88.2	22	12 PCT-US03-01814-6	Sequence 6, Appl1
39	19.4	88.2	22	12 US-08-627-967-6	Sequence 6, Appl1
40	19.4	88.2	22	13 US-08-751-384-6	Sequence 6, Appl1
41	19.4	88.2	22	47 US-10-054-429A-6	Sequence 6, Appl1
42	19	86.4	19	2 PCT-US03-05190-420	Sequence 420, App
43	19	86.4	19	2 PCT-US03-05190-429	Sequence 429, App
44	19	86.4	19	2 PCT-US03-05190-440	Sequence 440, App
45	19	86.4	19	2 PCT-US03-05190-466	Sequence 466, App

ALIGNMENTS

```
RESULT 1
US-08-478-464-6
; Sequence 6, Application US/08478464
; GENERAL INFORMATION:
; APPLICANT: Cohen, Aharon S.
; APPLICANT: Bourque, Andre
; APPLICANT: Vilenchik, Maria
; TITLE OF INVENTION: Method for Analyzing
; TITLE OF INVENTION: Oligonucleotide Analogs
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Lapin & Kusner
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,464
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-012DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/330-1300
; TELEFAX: 617/330-1311
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; US-08-478-464-6

Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTCT 22
   |||||
Db 1 TCGACCCATCTCTCTCTCT 22

RESULT 2
US-08-914-827-5
; Sequence 5, Application US/08914827
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Nudhir
; TITLE OF INVENTION: NOVEL HIV-SPECIFIC SYNTHETIC
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESS: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States Of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/914,827
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-914-827-5

```

```

Query Match      100.0%; Score 22; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TCGACCCATCTCTCTCTCT 22
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Db 1 TCGACCCATCTCTCTCTCT 22

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RESULT 3

```

US-09-837-806-5
Sequence 5, Application US/09837806
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: NOVEL HIV-SPECIFIC SYNTHETIC OLIGONUCLEOTIDES AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/837,806
FILING DATE: 30-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/914,827
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-5000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: YES

```

```

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-837-806-5

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Query Match      100.0%; Score 22; DB 36; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TCGACCCATCTCTCTCTCT 22
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Db 1 TCGACCCATCTCTCTCTCT 22

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RESULT 4

```

US-09-837-806A-5
Sequence 5, Application US/09837806A
GENERAL INFORMATION:
APPLICANT: AGRAMAL, SUDHIR
TITLE OF INVENTION: NOVEL HIV-SPECIFIC SYNTHETIC OLIGONUCLEOTIDES AND METHODS OF THEIR USE
FILE REFERENCE: HYZ-069CN
CURRENT APPLICATION NUMBER: US/09/837,806A
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 08/914,827
PRIOR FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-837-806A-5

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Query Match      100.0%; Score 22; DB 36; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 TCGACCCATCTCTCTCTCT 22
    |||||
Db 1 TCGACCCATCTCTCTCTCT 22

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RESULT 5

```

US-09-896-692B-5
Sequence 5, Application US/09896692B
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: NOVEL HIV-SPECIFIC SYNTHETIC OLIGONUCLEOTIDES AND METHODS OF THEIR USE
FILE REFERENCE: 47508.556 (HYZ-069)
CURRENT APPLICATION NUMBER: US/09/896,692B
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 08/914,827
PRIOR FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: synthetic modified antisense oligonucleotide
US-09-896-692B-5

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```

Query Match      100.0%; Score 22; DB 38; Length 22;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 TCGACCCATCTCTCTCTCT 22
    |||||
Db 1 TCGACCCATCTCTCTCTCT 22

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RESULT 6
US-08-478-464-7
Sequence 7, Application US/08478464
GENERAL INFORMATION:
APPLICANT: Cohen, Aharon S.
APPLICANT: Bourque, Andre
APPLICANT: Vilenchik, Maria
TITLE OF INVENTION: Method for Analyzing
TITLE OF INVENTION: Oligonucleotide Analogs
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusner
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,464
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-012DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/330-1310
TELEFAX: 617/330-1311
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
US-08-478-464-7

Query Match 95.5%; Score 21; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGCACCATCTCTCTCTCT 22
Db 1 CGCACCATCTCTCTCTCT 21

RESULT 7
US-08-914-827-1
Sequence 1, Application US/08914827
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: NOVEL HIV-SPECIFIC SYNTHETIC
TITLE OF INVENTION: OLIGONUCLEOTIDES AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,827
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA/RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-914-827-1

Query Match 95.5%; Score 21; DB 15; Length 21;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGACCATCTCTCTCTCT 21
Db 1 UCGACCATCTCTCTCT 21

RESULT 8
US-08-914-827-2
Sequence 2, Application US/08914827
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: NOVEL HIV-SPECIFIC SYNTHETIC
TITLE OF INVENTION: OLIGONUCLEOTIDES AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,827
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-914-827-2

Query Match 95.5%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGCACCATCTCTCTCTCT 21
Db 1 CGCACCATCTCTCTCTCT 21

RESULT 9
US-08-914-827-3
Sequence 3, Application US/08914827

GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: NOVEL HIV-SPECIFIC SYNTHETIC
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,827
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA/RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-914-827-3

Query Match 95.5%; Score 21; DB 15; Length 21;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CGCACCATCTCTCTCTCT 22
Db 1 CGCACCATCTCTCTCTCT 21

RESULT 10
US-08-914-827-4
Sequence 4, Application US/08914827
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: NOVEL HIV-SPECIFIC SYNTHETIC
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston

STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,827
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-914-827-4

Query Match 95.5%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CGCACCATCTCTCTCTCT 22
Db 1 CGCACCATCTCTCTCTCT 21

RESULT 11
US-08-914-827-6
Sequence 6, Application US/08914827
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: NOVEL HIV-SPECIFIC SYNTHETIC
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,827
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA/RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-914-827-6

Query Match 95.5%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTC 21
:|||||
DB 1 TCGACCCATCTCTCTCTTC 21

RESULT 12
US-09-708-786-2
; Sequence 2, Application US/09708786
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: Potentiation of Prodrug Efficacy
; FILE REFERENCE: 47508.700US
; CURRENT APPLICATION NUMBER: US/09/708,786
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30687
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent version 3.0
; SEQ ID NO: 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: oligonucleotide sequence
US-09-708-786-2

Query Match 95.5%; Score 21; DB 32; Length 21;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTC 21
:|||||
DB 1 UCGACCCATCTCTCTCTTC 21

RESULT 13
US-09-805-761-35
; Sequence 35, Application US/09805761
; GENERAL INFORMATION:
; APPLICANT: G111, Parkesh
; APPLICANT: Masood, Rizwan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; FILE REFERENCE: 21327-701CON2
; CURRENT APPLICATION NUMBER: US/09/805,761
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 35
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Scrambled mixed backbone oligonucleotides,
OTHER INFORMATION: nucleotides 1-4 and 18-21 and 2'0
OTHER INFORMATION: methylribonucleosides
US-09-805-761-35

Query Match 95.5%; Score 21; DB 35; Length 21;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTC 21
:|||||
DB 1 UCGACCCATCTCTCTCTTC 21

RESULT 14
US-09-837-806-1
; Sequence 1, Application US/09837806
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; TITLE OF INVENTION: NOVEL HIV-SPECIFIC SYNTHETIC
; OLIGONUCLEOTIDES AND METHODS OF THEIR USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States Of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/837,806
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/914,827
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Keirner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-069
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA/RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-837-806-1

Query Match 95.5%; Score 21; DB 36; Length 21;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGACCCATCTCTCTCTTC 21
:|||||
DB 1 UCGACCCATCTCTCTCTTC 21

RESULT 15
US-09-837-806-2
; Sequence 2, Application US/09837806
; GENERAL INFORMATION:

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APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: NOVEL HIV-SPECIFIC SYNTHETIC
OLIGONUCLEOTIDES AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States Of America
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/837,806
FILING DATE: 30-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/914,827
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-837-806-2

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Query Match      95.5%; Score 21; DB 36; Length 21;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 TCGACCCATCTCTCCTTC 21
      |||||
Db      1 TCGACCCATCTCTCCTTC 21

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